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<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> 446.001

<140> 09/786,880

<141> 2001-06-01

<150> PCT/EP99/07376

<151> 1999-09-13

<150> EP 98402255.8

<151> 1998-09-11

<160> 72

<170> PatentIn Ver. 2.1

<210> 1

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic probe

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cctgtcaaag ataataatttt gaaatttgat caaattaatc ataaatctcc tactttgatt 180
atgggtatat tgaatatgac tcctgattca tttagtgatg gtgggaaaca ttttgaaaa 240
gaactagata atattgtgaa gcaggcagag aaattagtcg gtgaggggtgc tacgattatt 300
gacattggag gagtttccac acgaccagga agtggtgaac ccactgagga agaagaattg 360
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 <213> *Candida albicans*

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 <222> (1)..(2364)

<220>
 <221> gene
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 <223> gene CaNL256

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 ata act ggt aaa gat gcc tgg aat cgg cca aca cca caa cca atc act 96
 Ile Thr Gly Lys Asp Ala Trp Asn Arg Pro Thr Pro Gln Pro Ile Thr
 20 25 30
 ata tca tta tct ttc aat act gat ttc cat aag gca tcg gaa ttg gat 144
 Ile Ser Leu Ser Phe Asn Thr Asp Phe His Lys Ala Ser Glu Leu Asp
 35 40 45
 aat ttg aaa tac tca att aat tat gct gtt att acc aga aat gta act 192
 Asn Leu Lys Tyr Ser Ile Asn Tyr Ala Val Ile Thr Arg Asn Val Thr
 50 55 60
 gaa ttt atg aaa tca aat gag cat tta aat ttc aag tca tta gga aat 240
 Glu Phe Met Lys Ser Asn Glu His Leu Asn Phe Lys Ser Leu Gly Asn
 65 70 75 80
 att gct caa gca att agt gat att gga tta gat caa tct aga ggt ggt 288
 Ile Ala Gln Ala Ile Ser Asp Ile Gly Leu Asp Gln Ser Arg Gly Gly
 85 90 95
 gga tct att gtg gat gtg acg ata aaa agt ttg aaa tca gaa ata aga 336
 Gly Ser Ile Val Asp Val Thr Ile Lys Ser Leu Lys Ser Glu Ile Arg
 100 105 110
 gct gaa agt gtc gaa tat aaa att aat aga aac act ttg ggt caa ccc 384
 Ala Glu Ser Val Glu Tyr Lys Ile Asn Arg Asn Thr Leu Gly Gln Pro
 115 120 125
 gtt cca tta gat att ttc caa gtt aat aaa ttg aga tta ttg acg att 432
 Val Pro Leu Asp Ile Phe Gln Val Asn Lys Leu Arg Leu Leu Thr Ile
 130 135 140
 att gga gtt ttc aca ttt gaa aga tta caa aaa caa ata gtt gat gtt 480
 Ile Gly Val Phe Thr Phe Glu Arg Leu Gln Lys Gln Ile Val Asp Val
 145 150 155 160

gat ttg caa ttt aaa att gaa cct aat tcc aat tta tat ttc cat caa	528
Asp Leu Gln Phe Lys Ile Glu Pro Asn Ser Asn Leu Tyr Phe His Gln	
165 170 175	
ata att gct gat att gtt tca tac gtg gaa tca tct aat ttc aaa act	576
Ile Ile Ala Asp Ile Val Ser Tyr Val Glu Ser Ser Asn Phe Lys Thr	
180 185 190	
gta gaa gca ttg gtg tct aag att ggt caa ttg aca ttt cag aaa tat	624
Val Glu Ala Leu Val Ser Lys Ile Gly Gln Leu Thr Phe Gln Lys Tyr	
195 200 205	
gac gga gta gct gaa gtt gtt gct act gtc act aaa ccg aat gca ttt	672
Asp Gly Val Ala Glu Val Val Ala Thr Val Thr Lys Pro Asn Ala Phe	
210 215 220	
agt cat gtt gaa ggt gtt gga gta tca tct acc atg gtc aaa gac aat	720
Ser His Val Glu Gly Val Gly Val Ser Ser Thr Met Val Lys Asp Asn	
225 230 235 240	
ttc aaa gat atg gaa cca gtt aaa ttt gaa aac aca att gct caa act	768
Phe Lys Asp Met Glu Pro Val Lys Phe Glu Asn Thr Ile Ala Gln Thr	
245 250 255	
aat aga gca ttc aat tta cct gtt gaa aat gag aaa act gag gat tat	816
Asn Arg Ala Phe Asn Leu Pro Val Glu Asn Glu Lys Thr Glu Asp Tyr	
260 265 270	
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Thr Gly Tyr His Thr Ala Phe Ile Ala Phe Gly Ser Asn Thr Gly Asn	
275 280 285	
caa gta gaa aat att acc aat tca ttc gaa ttg ttg caa aaa tat gga	912
Gln Val Glu Asn Ile Thr Asn Ser Phe Glu Leu Leu Gln Lys Tyr Gly	
290 295 300	
atc acc ata gaa gca act tca tca ttg tac att tct aaa cca atg tat	960
Ile Thr Ile Glu Ala Thr Ser Ser Leu Tyr Ile Ser Lys Pro Met Tyr	
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tac ttg gat caa cca gat ttt ttc aat gga gta att aaa gtg aat ttc	1008
Tyr Leu Asp Gln Pro Asp Phe Phe Asn Gly Val Ile Lys Val Asn Phe	
325 330 335	
caa aac att tca cct ttc cag ttg ttg aaa att cta aaa gat att gaa	1056
Gln Asn Ile Ser Pro Phe Gln Leu Leu Lys Ile Leu Lys Asp Ile Glu	
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tat aaa cat tta gaa agg aaa aaa gac ttt gat aat ggg ccc aga tca	1104
Tyr Lys His Leu Glu Arg Lys Lys Asp Phe Asp Asn Gly Pro Arg Ser	
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Asn Leu Ile Ile Pro His Lys Ser Met Leu Glu Arg Thr Phe Val Leu	
385 390 395 400	
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Gln Pro Leu Cys Glu Val Leu Pro Pro Asp Tyr Ile His Pro Ile Ser	
405 410 415	
gca gaa agt ttg cat agc cat tta caa caa tta ata aat gat aaa cct	1296
Ala Glu Ser Leu His Ser His Leu Gln Gln Leu Ile Asn Asp Lys Pro	
420 425 430	
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Gln Glu Thr Val Gln Glu Ser Ser Asp Leu Leu Gln Phe Ile Pro Val	
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tct aga ttg cct gtc aaa gat aat att ttg aaa ttt gat caa att aat	1392
Ser Arg Leu Pro Val Lys Asp Asn Ile Leu Lys Phe Asp Gln Ile Asn	
450 455 460	
cat aaa tct cct act ttg att atg ggt ata ttg aat atg act cct gat	1440
His Lys Ser Pro Thr Leu Ile Met Gly Ile Leu Asn Met Thr Pro Asp	
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Ser Phe Ser Asp Gly Lys His Phe Gly Lys Glu Leu Asp Asn Thr	
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Val Lys Gln Ala Glu Lys Leu Val Ser Glu Gly Ala Thr Ile Ile Asp	
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Ile Gly Gly Val Ser Thr Arg Pro Gly Ser Val Glu Pro Thr Glu Glu	
515 520 525	
gaa gaa ttg gaa cgt gtg att cca tta att aaa gct att cgt caa tca	1632
Glu Glu Leu Glu Arg Val Ile Pro Leu Ile Lys Ala Ile Arg Gln Ser	
530 535 540	
ctg aac cct gat tta ctg aag gtg ttg att tcg gtt gat act tat cgt	1680
Leu Asn Pro Asp Leu Leu Lys Val Leu Ile Ser Val Asp Thr Tyr Arg	
545 550 555 560	
agg aac gtt gct gaa caa agt tta ctt gtg ggt gct gac ata atc aac	1728
Arg Asn Val Ala Glu Gln Ser Leu Leu Val Gly Ala Asp Ile Ile Asn	
565 570 575	

gat atc tca atg ggc aaa tat gat gaa aaa ata ttt gat gtg gtt gct Asp Ile Ser Met Gly Lys Tyr Asp Glu Lys Ile Phe Asp Val Val Ala	1776
580 585 590	
aaa tac gga tgt cct tat atc atg aat cat act cga gga tca cct aaa Lys Tyr Gly Cys Pro Tyr Ile Met Asn His Thr Arg Gly Ser Pro Lys	1824
595 600 605	
acc atg tct aaa ttg acc aat tat gaa tca aat aca aat gat gat att Thr Met Ser Lys Leu Thr Asn Tyr Glu Ser Asn Thr Asn Asp Asp Ile	1872
610 615 620	
atc gaa tat ata att gat cct aaa tta gga cat caa gaa ttg gat ttg Ile Glu Tyr Ile Ile Asp Pro Lys Leu Gly His Gln Glu Leu Asp Leu	1920
625 630 635 640	
tca cct gaa atc aag aat tta ctc aat gga atc agt cgt gaa ttg agt Ser Pro Glu Ile Lys Asn Leu Leu Asn Gly Ile Ser Arg Glu Leu Ser	1968
645 650 655	
tta caa atg ttt aaa gcc atg gct aaa gga gtg aaa aaa tgg caa att Leu Gln Met Phe Lys Ala Met Ala Lys Gly Val Lys Lys Trp Gln Ile	2016
660 665 670	
att ttg gat cct ggt att gga ttt gct aaa aat ttg aat caa aat tta Ile Leu Asp Pro Gly Ile Gly Phe Ala Lys Asn Leu Asn Gln Asn Leu	2064
675 680 685	
gca gtt att cgt aat gcc tgc ttt ttt aaa aaa tat tct att caa att Ala Val Ile Arg Asn Ala Ser Phe Phe Lys Lys Tyr Ser Ile Gln Ile	2112
690 695 700	
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705 710 715 720	
aat ggt gct tgt gtt ttg gtg ggg aca tca aga aag aag ttt ttg ggg Asn Gly Ala Cys Val Leu Val Gly Thr Ser Arg Lys Lys Phe Leu Gly	2208
725 730 735	
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740 745 750	
gca aca gtg tct gcg tgt att gaa caa aac act gat att gta aga gtt Ala Thr Val Ser Ala Cys Ile Glu Gln Asn Thr Asp Ile Val Arg Val	2304
755 760 765	
cat gat gtt aaa gaa atg aaa gat gta gta tgt ata agt gat gca att His Asp Val Lys Glu Met Lys Asp Val Val Cys Ile Ser Asp Ala Ile	2352
770 775 780	

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 Tyr Lys Asn Val
 785

2367

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 <213> Candida albicans

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 35 40 45
 Asn Leu Lys Tyr Ser Ile Asn Tyr Ala Val Ile Thr Arg Asn Val Thr
 50 55 60
 Glu Phe Met Lys Ser Asn Glu His Leu Asn Phe Lys Ser Leu Gly Asn
 65 70 75 80
 Ile Ala Gln Ala Ile Ser Asp Ile Gly Leu Asp Gln Ser Arg Gly Gly
 85 90 95
 Gly Ser Ile Val Asp Val Thr Ile Lys Ser Leu Lys Ser Glu Ile Arg
 100 105 110
 Ala Glu Ser Val Glu Tyr Lys Ile Asn Arg Asn Thr Leu Gly Gln Pro
 115 120 125
 Val Pro Leu Asp Ile Phe Gln Val Asn Lys Leu Arg Leu Leu Thr Ile
 130 135 140
 Ile Gly Val Phe Thr Phe Glu Arg Leu Gln Lys Gln Ile Val Asp Val
 145 150 155 160
 Asp Leu Gln Phe Lys Ile Glu Pro Asn Ser Asn Leu Tyr Phe His Gln
 165 170 175
 Ile Ile Ala Asp Ile Val Ser Tyr Val Glu Ser Ser Asn Phe Lys Thr
 180 185 190
 Val Glu Ala Leu Val Ser Lys Ile Gly Gln Leu Thr Phe Gln Lys Tyr
 195 200 205
 Asp Gly Val Ala Glu Val Val Ala Thr Val Thr Lys Pro Asn Ala Phe
 210 215 220

Ser His Val Glu Gly Val Gly Val Ser Ser Thr Met Val Lys Asp Asn
 225 230 235 240
 Phe Lys Asp Met Glu Pro Val Lys Phe Glu Asn Thr Ile Ala Gln Thr
 245 250 255
 Asn Arg Ala Phe Asn Leu Pro Val Glu Asn Glu Lys Thr Glu Asp Tyr
 260 265 270
 Thr Gly Tyr His Thr Ala Phe Ile Ala Phe Gly Ser Asn Thr Gly Asn
 275 280 285
 Gln Val Glu Asn Ile Thr Asn Ser Phe Glu Leu Leu Gln Lys Tyr Gly
 290 295 300
 Ile Thr Ile Glu Ala Thr Ser Ser Leu Tyr Ile Ser Lys Pro Met Tyr
 305 310 315 320
 Tyr Leu Asp Gln Pro Asp Phe Phe Asn Gly Val Ile Lys Val Asn Phe
 325 330 335
 Gln Asn Ile Ser Pro Phe Gln Leu Leu Lys Ile Leu Lys Asp Ile Glu
 340 345 350
 Tyr Lys His Leu Glu Arg Lys Lys Asp Phe Asp Asn Gly Pro Arg Ser
 355 360 365
 Ile Asp Leu Asp Ile Ile Leu Tyr Asp Asp Leu Gln Leu Asn Thr Glu
 370 375 380
 Asn Leu Ile Ile Pro His Lys Ser Met Leu Glu Arg Thr Phe Val Leu
 385 390 395 400
 Gln Pro Leu Cys Glu Val Leu Pro Pro Asp Tyr Ile His Pro Ile Ser
 405 410 415
 Ala Glu Ser Leu His Ser His Leu Gln Gln Leu Ile Asn Asp Lys Pro
 420 425 430
 Gln Glu Thr Val Gln Glu Ser Ser Asp Leu Leu Gln Phe Ile Pro Val
 435 440 445
 Ser Arg Leu Pro Val Lys Asp Asn Ile Leu Lys Phe Asp Gln Ile Asn
 450 455 460
 His Lys Ser Pro Thr Leu Ile Met Gly Ile Leu Asn Met Thr Pro Asp
 465 470 475 480
 Ser Phe Ser Asp Gly Gly Lys His Phe Gly Lys Glu Leu Asp Asn Thr
 485 490 495
 Val Lys Gln Ala Glu Lys Leu Val Ser Glu Gly Ala Thr Ile Ile Asp
 500 505 510

Ile Gly Gly Val Ser Thr Arg Pro Gly Ser Val Glu Pro Thr Glu Glu
 515 520 525
 Glu Glu Leu Glu Arg Val Ile Pro Leu Ile Lys Ala Ile Arg Gln Ser
 530 535 540
 Leu Asn Pro Asp Leu Leu Lys Val Leu Ile Ser Val Asp Thr Tyr Arg
 545 550 555 560
 Arg Asn Val Ala Glu Gln Ser Leu Leu Val Gly Ala Asp Ile Ile Asn
 565 570 575
 Asp Ile Ser Met Gly Lys Tyr Asp Glu Lys Ile Phe Asp Val Val Ala
 580 585 590
 Lys Tyr Gly Cys Pro Tyr Ile Met Asn His Thr Arg Gly Ser Pro Lys
 595 600 605
 Thr Met Ser Lys Leu Thr Asn Tyr Glu Ser Asn Thr Asn Asp Asp Ile
 610 615 620
 Ile Glu Tyr Ile Ile Asp Pro Lys Leu Gly His Gln Glu Leu Asp Leu
 625 630 635 640
 Ser Pro Glu Ile Lys Asn Leu Leu Asn Gly Ile Ser Arg Glu Leu Ser
 645 650 655
 Leu Gln Met Phe Lys Ala Met Ala Lys Gly Val Lys Lys Trp Gln Ile
 660 665 670
 Ile Leu Asp Pro Gly Ile Gly Phe Ala Lys Asn Leu Asn Gln Asn Leu
 675 680 685
 Ala Val Ile Arg Asn Ala Ser Phe Phe Lys Lys Tyr Ser Ile Gln Ile
 690 695 700
 Asn Glu Arg Val Asp Asp Val Thr Ile Lys His Lys Tyr Leu Ser Phe
 705 710 715 720
 Asn Gly Ala Cys Val Leu Val Gly Thr Ser Arg Lys Lys Phe Leu Gly
 725 730 735
 Thr Leu Thr Gly Asn Glu Val Pro Leu Asp Arg Val Phe Gly Thr Gly
 740 745 750
 Ala Thr Val Ser Ala Cys Ile Glu Gln Asn Thr Asp Ile Val Arg Val
 755 760 765
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 Tyr Lys Asn Val
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic probe

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 tttgtgcaac cattacccaa tagacacatt gtcgcggaaa gtggacgatg gtttgaagtt 180
 aatgtgggga attggaaacc aagttatcca actcatttat ttatatataa tgatttaatt 240
 ttaattgccg ttaaaaaatc atcatctagt agtcaggaac ctactacagg gggaagtaat 300
 ggtggttcaa aatcgagatt acaagcgggt caatggtggc ccttaactca agtatcatta 360
 caacaaatca aatcaccgaa aaaagatgac gataagatgt attttatcaa tcttaaatcc 420
 aaatctttta gttatgtata cctgacggat cgttatgatc attttgtgaa agttacggaa 480
 gcatttaata aaggtagaaa tgaaatgatt caaagtgaag gattattaga ttcaagactt 540
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 <222> (1)..(2373)

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 <223> gene CaBR102

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Asn	Arg	Lys	Ser	Arg	Ala	Val	Trp	Gln	Asn	Asn	Asn	Thr	Ser	Thr	His	
		20						25					30			
aat	aat	cct	tat	gct	aat	tta	agc	act	ggg	gaa	aaa	agt	agg	agt	cgc	144
Asn	Asn	Pro	Tyr	Ala	Asn	Leu	Ser	Thr	Gly	Glu	Lys	Ser	Arg	Ser	Arg	
		35					40					45				
cat	aac	act	ggg	agt	tct	tat	gtt	tct	cca	tat	ggc	ggc	ggg	aat	gga	192
His	Asn	Thr	Gly	Ser	Ser	Tyr	Val	Ser	Pro	Tyr	Gly	Gly	Gly	Asn	Gly	
	50					55					60					
gag	gag	aat	gct	tat	act	ggg	aat	aac	aac	aaa	tca	aat	act	agt	ggg	240
Glu	Glu	Asn	Ala	Tyr	Thr	Gly	Asn	Asn	Asn	Lys	Ser	Asn	Thr	Ser	Gly	
	65				70					75					80	
aat	tta	tta	caa	gtt	cct	gga	gca	gga	gga	gga	gga	gat	ttg	aat	tct	288
Asn	Leu	Leu	Gln	Val	Pro	Gly	Ala	Gly	Gly	Gly	Gly	Asp	Leu	Asn	Ser	
			85					90						95		
aat	aag	aaa	caa	agt	cga	aga	atg	agt	att	cat	gta	tca	gct	cgt	caa	336
Asn	Lys	Lys	Gln	Ser	Arg	Arg	Met	Ser	Ile	His	Val	Ser	Ala	Arg	Gln	
		100					105						110			
cat	gga	aga	tca	ttt	tca	caa	act	ggg	cca	att	gat	atg	gca	aat	tta	384
His	Gly	Arg	Ser	Phe	Ser	Gln	Thr	Gly	Pro	Ile	Asp	Met	Ala	Asn	Leu	
		115				120						125				
ccg	gca	tta	cct	aaa	ata	ggg	ggg	gtt	act	act	agt	ggg	gtt	ggc	ggg	432
Pro	Ala	Leu	Pro	Lys	Ile	Gly	Gly	Val	Thr	Thr	Ser	Gly	Val	Gly	Gly	
	130					135					140					
gct	ggg	ggg	gat	gtt	atg	aca	agg	act	ggg	gga	ttg	acg	ata	gaa	caa	480
Ala	Gly	Gly	Asp	Val	Met	Thr	Arg	Thr	Gly	Gly	Leu	Thr	Ile	Glu	Gln	
	145				150				155					160		
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Lys	Ile	Phe	Lys	Glu	Leu	Ser	Gln	Gly	Ser	Ala	Ala	Glu	Val	Asp	Asp	
			165					170					175			
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Tyr	Tyr	Lys	Thr	Leu	Leu	Lys	Gln	Lys	Asn	Leu	Ile	Thr	Arg	Asp	Ile	
		180					185						190			
aag	gat	aat	att	aat	cag	aat	caa	aaa	aat	att	tta	caa	tta	aca	aaa	624
Lys	Asp	Asn	Ile	Asn	Gln	Asn	Gln	Lys	Asn	Ile	Leu	Gln	Leu	Thr	Lys	
		195					200					205				
gac	ttg	aaa	gag	acc	caa	gaa	gaa	ttg	att	gaa	ttg	aga	gga	acc	act	672
Asp	Leu	Lys	Glu	Thr	Gln	Glu	Glu	Leu	Ile	Glu	Leu	Arg	Gly	Thr	Thr	
	210					215					220					

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Lys Glu Leu Tyr Glu Val Leu Gly Tyr Phe	Lys Glu Ser Ala Gln Arg	
225	235 240	
230		
aga tta gaa ttg gaa ttt gaa cca gaa aca	caa aaa gaa ctt cat ctg	768
Arg Leu Glu Leu Glu Phe Glu Pro Glu Thr	Gln Lys Glu Leu His Leu	
245	250 255	
cct caa aaa agt aat caa ttg ggt att cct	agt aat aaa aag aaa gat	816
Pro Gln Lys Ser Asn Gln Leu Gly Ile	Pro Ser Asn Lys Lys Lys Asp	
260	265 270	
cga tca tca att atg gtg ctt aaa aaa atg	tgg gat tct caa tta caa	864
Arg Ser Ser Ile Met Val Leu Lys Lys Met	Trp Asp Ser Gln Leu Gln	
275	280 285	
tca tta ttt aaa cat gtt gac ggt gca tca	aaa ttt gtc caa cca tta	912
Ser Leu Phe Lys His Val Asp Gly Ala Ser	Lys Phe Val Gln Pro Leu	
290	295 300	
ccc aat aga cac att gtc gcg gaa agt gga	cga tgg ttt gaa gtt aat	960
Pro Asn Arg His Ile Val Ala Glu Ser Gly	Arg Trp Phe Glu Val Asn	
305	310 315 320	
gtg ggg aat tgg aaa cca agt tat cca act	cat tta ttt ata ttt aat	1008
Val Gly Asn Trp Lys Pro Ser Tyr Pro Thr	His Leu Phe Ile Phe Asn	
325	330 335	
gat tta att tta att act gtt aaa aaa tca	tca tct agt agt cag gaa	1056
Asp Leu Ile Leu Ile Thr Val Lys Lys Ser	Ser Ser Ser Ser Gln Glu	
340	345 350	
cct act aca ggg gga agt aat ggt ggt tca	aaa tcg aga tta caa gcg	1104
Pro Thr Thr Gly Gly Ser Asn Gly Gly Ser	Lys Ser Arg Leu Gln Ala	
355	360 365	
gtt caa tgt tgg ccc tta act caa gta tca	tta caa caa atc aaa tca	1152
Val Gln Cys Trp Pro Leu Thr Gln Val Ser	Leu Gln Gln Ile Lys Ser	
370	375 380	
ccg aaa aaa gat gac gat aag atg tat ttt	atc aat ctt aaa tcc aaa	1200
Pro Lys Lys Asp Asp Asp Lys Met Tyr Phe	Ile Asn Leu Lys Ser Lys	
385	390 395 400	
tct tta agt tat gta tac ctg acg gat cgt	tat gat cat ttt gtg aaa	1248
Ser Leu Ser Tyr Val Tyr Leu Thr Asp Arg	Tyr Asp His Phe Val Lys	
405	410 415	
gtt acg gaa gca ttt aat aaa ggt aga aat	gaa atg att caa agt gaa	1296
Val Thr Glu Ala Phe Asn Lys Gly Arg Asn	Glu Met Ile Gln Ser Glu	
420	425 430	

aga tta tta gat tca aga ctt tca tct cct tca aat aat aat gga gat	1344
Arg Leu Leu Asp Ser Arg Leu Ser Ser Pro Ser Asn Asn Asn Gly Asp	
435 440 445	
tct aaa gaa gag aaa cga caa tta cgg gaa tca tta aga aac tca ggc	1392
Ser Lys Glu Glu Lys Arg Gln Leu Arg Glu Ser Leu Arg Asn Ser Gly	
450 455 460	
aat tat aaa gaa gga gtt act gat gat gcc ggt gga gct gca act ggt	1440
Asn Tyr Lys Glu Gly Val Thr Asp Asp Ala Gly Gly Ala Ala Thr Gly	
465 470 475 480	
ggg ggt agg aaa agt gcc ggt act cct aat aga aat agt act gat tac	1488
Gly Gly Arg Lys Ser Ala Gly Thr Pro Asn Arg Asn Ser Thr Asp Tyr	
485 490 495	
gtt tta cat gat ata tct gct cga gta cat tca cgt aat cga tca caa	1536
Val Leu His Asp Ile Ser Ala Arg Val His Ser Arg Asn Arg Ser Gln	
500 505 510	
gat tta ggg aat aat ttc aaa tta gct aat aat ggg aaa tca caa ttt	1584
Asp Leu Gly Asn Asn Phe Lys Leu Ala Asn Asn Gly Lys Ser Gln Phe	
515 520 525	
ttc aat gaa atc aaa act tta gaa gat cga tta gat gat gtt gac gtt	1632
Phe Asn Glu Ile Lys Thr Leu Glu Asp Arg Leu Asp Asp Val Asp Val	
530 535 540	
gaa ata tcg cat aat caa tat gct gaa gcc gtg gaa tta ata tca ata	1680
Glu Ile Ser His Asn Gln Tyr Ala Glu Ala Val Glu Leu Ile Ser Ile	
545 550 555 560	
att gaa tct aaa tta cgt aat att gaa aat gca tta act aat caa cgt	1728
Ile Glu Ser Lys Leu Arg Asn Ile Glu Asn Ala Leu Thr Asn Gln Arg	
565 570 575	
aat gga ggt aaa aat gtc aat att gct gat gaa tta tta ctt tta gat	1776
Asn Gly Gly Lys Asn Val Asn Ile Ala Asp Glu Leu Leu Leu Leu Asp	
580 585 590	
gta tca aaa ttg aaa att aaa aat cgg aaa gaa aat gta tct aat gga	1824
Val Ser Lys Leu Lys Ile Lys Asn Arg Lys Glu Asn Val Ser Asn Gly	
595 600 605	
tta ata ttt gat tta caa cat aat ata gct aaa ctt aaa caa gat gat	1872
Leu Ile Phe Asp Leu Gln His Asn Ile Ala Lys Leu Lys Gln Asp Asp	
610 615 620	
att gat aat att ttg acg tta ttt gat aat tta gag caa tta gat cga	1920
Ile Asp Asn Ile Leu Thr Leu Phe Asp Asn Leu Glu Gln Leu Asp Arg	
625 630 635 640	

ggg gtt caa gga tat ttg gat tca atg tca gct tat tta tca act aca 1968
 Gly Val Gln Gly Tyr Leu Asp Ser Met Ser Ala Tyr Leu Ser Thr Thr
 645 650 655

gta tca aaa tta att gtt ggt tta caa gga tca acg aaa atc gat gtt 2016
 Val Ser Lys Leu Ile Val Gly Leu Gln Gly Ser Thr Lys Ile Asp Val
 660 665 670

gtt aat tat ctt tcc aat tta atg gtt att aat gta tgc att gtg aaa 2064
 Val Asn Tyr Leu Ser Asn Leu Met Val Ile Asn Val Ser Ile Val Lys
 675 680 685

cgt aca att caa act tat gaa caa ata att gct cca att tta aaa cgt 2112
 Arg Thr Ile Gln Thr Tyr Glu Gln Ile Ile Ala Pro Ile Leu Lys Arg
 690 695 700

cat ggt gat gtt gat tca agt gga ttg att aat tgg tgt att gat gaa 2160
 His Gly Asp Val Asp Ser Ser Gly Leu Ile Asn Trp Cys Ile Asp Glu
 705 710 715 720

ttt act aaa ctt tgt aaa caa att aaa aaa cat ttg tat gga aca ttg 2208
 Phe Thr Lys Leu Cys Lys Gln Ile Lys Lys His Leu Tyr Gly Thr Leu
 725 730 735

ttg ata tct tct ggg att aat atg gaa act gat gaa cca att tat aaa 2256
 Leu Ile Ser Ser Gly Ile Asn Met Glu Thr Asp Glu Pro Ile Tyr Lys
 740 745 750

gtt aaa gaa aga aaa tta tat gat aat ttc ttg aag att atg caa cca 2304
 Val Lys Glu Arg Lys Leu Tyr Asp Asn Phe Leu Lys Ile Met Gln Pro
 755 760 765

caa ttg gaa gaa tta aaa ctg gtg gga tta aat gtt gat tat ata ttt 2352
 Gln Leu Glu Glu Leu Lys Leu Val Gly Leu Asn Val Asp Tyr Ile Phe
 770 775 780

gag tct ata tta aat ctt gaa 2373
 Glu Ser Ile Leu Asn Leu Glu
 785 790

<210> 6
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 <212> PRT
 <213> Candida albicans

<400> 6
 Met Asp Asn Leu Asp Pro Asn Ser Ser Leu Gln Val Glu Lys Leu Arg
 1 5 10 15
 Asn Arg Lys Ser Arg Ala Val Trp Gln Asn Asn Asn Thr Ser Thr His
 20 25 30

Asn	Asn	Pro	Tyr	Ala	Asn	Leu	Ser	Thr	Gly	Glu	Lys	Ser	Arg	Ser	Arg	35	40	45
His	Asn	Thr	Gly	Ser	Ser	Tyr	Val	Ser	Pro	Tyr	Gly	Gly	Gly	Asn	Gly	50	55	60
Glu	Glu	Asn	Ala	Tyr	Thr	Gly	Asn	Asn	Asn	Lys	Ser	Asn	Thr	Ser	Gly	65	70	75
Asn	Leu	Leu	Gln	Val	Pro	Gly	Ala	Gly	Gly	Gly	Gly	Asp	Leu	Asn	Ser	85	90	95
Asn	Lys	Lys	Gln	Ser	Arg	Arg	Met	Ser	Ile	His	Val	Ser	Ala	Arg	Gln	100	105	110
His	Gly	Arg	Ser	Phe	Ser	Gln	Thr	Gly	Pro	Ile	Asp	Met	Ala	Asn	Leu	115	120	125
Pro	Ala	Leu	Pro	Lys	Ile	Gly	Gly	Val	Thr	Thr	Ser	Gly	Val	Gly	Gly	130	135	140
Ala	Gly	Gly	Asp	Val	Met	Thr	Arg	Thr	Gly	Gly	Leu	Thr	Ile	Glu	Gln	145	150	155
Lys	Ile	Phe	Lys	Glu	Leu	Ser	Gln	Gly	Ser	Ala	Ala	Glu	Val	Asp	Asp	165	170	175
Tyr	Tyr	Lys	Thr	Leu	Leu	Lys	Gln	Lys	Asn	Leu	Ile	Thr	Arg	Asp	Ile	180	185	190
Lys	Asp	Asn	Ile	Asn	Gln	Asn	Gln	Lys	Asn	Ile	Leu	Gln	Leu	Thr	Lys	195	200	205
Asp	Leu	Lys	Glu	Thr	Gln	Glu	Glu	Leu	Ile	Glu	Leu	Arg	Gly	Thr	Thr	210	215	220
Lys	Glu	Leu	Tyr	Glu	Val	Leu	Gly	Tyr	Phe	Lys	Glu	Ser	Ala	Gln	Arg	225	230	235
Arg	Leu	Glu	Leu	Glu	Phe	Glu	Pro	Glu	Thr	Gln	Lys	Glu	Leu	His	Leu	245	250	255
Pro	Gln	Lys	Ser	Asn	Gln	Leu	Gly	Ile	Pro	Ser	Asn	Lys	Lys	Lys	Asp	260	265	270
Arg	Ser	Ser	Ile	Met	Val	Leu	Lys	Lys	Met	Trp	Asp	Ser	Gln	Leu	Gln	275	280	285
Ser	Leu	Phe	Lys	His	Val	Asp	Gly	Ala	Ser	Lys	Phe	Val	Gln	Pro	Leu	290	295	300
Pro	Asn	Arg	His	Ile	Val	Ala	Glu	Ser	Gly	Arg	Trp	Phe	Glu	Val	Asn	305	310	315
																		320

Val	Gly	Asn	Trp	Lys	Pro	Ser	Tyr	Pro	Thr	His	Leu	Phe	Ile	Phe	Asn	325	330	335
Asp	Leu	Ile	Leu	Ile	Thr	Val	Lys	Lys	Ser	Ser	Ser	Ser	Ser	Gln	Glu	340	345	350
Pro	Thr	Thr	Gly	Gly	Ser	Asn	Gly	Gly	Ser	Lys	Ser	Arg	Leu	Gln	Ala	355	360	365
Val	Gln	Cys	Trp	Pro	Leu	Thr	Gln	Val	Ser	Leu	Gln	Gln	Ile	Lys	Ser	370	375	380
Pro	Lys	Lys	Asp	Asp	Asp	Lys	Met	Tyr	Phe	Ile	Asn	Leu	Lys	Ser	Lys	385	390	395
Ser	Leu	Ser	Tyr	Val	Tyr	Leu	Thr	Asp	Arg	Tyr	Asp	His	Phe	Val	Lys	405	410	415
Val	Thr	Glu	Ala	Phe	Asn	Lys	Gly	Arg	Asn	Glu	Met	Ile	Gln	Ser	Glu	420	425	430
Arg	Leu	Leu	Asp	Ser	Arg	Leu	Ser	Ser	Pro	Ser	Asn	Asn	Asn	Gly	Asp	435	440	445
Ser	Lys	Glu	Glu	Lys	Arg	Gln	Leu	Arg	Glu	Ser	Leu	Arg	Asn	Ser	Gly	450	455	460
Asn	Tyr	Lys	Glu	Gly	Val	Thr	Asp	Asp	Ala	Gly	Gly	Ala	Ala	Thr	Gly	465	470	475
Gly	Gly	Arg	Lys	Ser	Ala	Gly	Thr	Pro	Asn	Arg	Asn	Ser	Thr	Asp	Tyr	485	490	495
Val	Leu	His	Asp	Ile	Ser	Ala	Arg	Val	His	Ser	Arg	Asn	Arg	Ser	Gln	500	505	510
Asp	Leu	Gly	Asn	Asn	Phe	Lys	Leu	Ala	Asn	Asn	Gly	Lys	Ser	Gln	Phe	515	520	525
Phe	Asn	Glu	Ile	Lys	Thr	Leu	Glu	Asp	Arg	Leu	Asp	Asp	Val	Asp	Val	530	535	540
Glu	Ile	Ser	His	Asn	Gln	Tyr	Ala	Glu	Ala	Val	Glu	Leu	Ile	Ser	Ile	545	550	555
Ile	Glu	Ser	Lys	Leu	Arg	Asn	Ile	Glu	Asn	Ala	Leu	Thr	Asn	Gln	Arg	565	570	575
Asn	Gly	Gly	Lys	Asn	Val	Asn	Ile	Ala	Asp	Glu	Leu	Leu	Leu	Leu	Asp	580	585	590
Val	Ser	Lys	Leu	Lys	Ile	Lys	Asn	Arg	Lys	Glu	Asn	Val	Ser	Asn	Gly	595	600	605

Leu Ile Phe Asp Leu Gln His Asn Ile Ala Lys Leu Lys Gln Asp Asp
 610 615 620

Ile Asp Asn Ile Leu Thr Leu Phe Asp Asn Leu Glu Gln Leu Asp Arg
 625 630 635 640

Gly Val Gln Gly Tyr Leu Asp Ser Met Ser Ala Tyr Leu Ser Thr Thr
 645 650 655

Val Ser Lys Leu Ile Val Gly Leu Gln Gly Ser Thr Lys Ile Asp Val
 660 665 670

Val Asn Tyr Leu Ser Asn Leu Met Val Ile Asn Val Ser Ile Val Lys
 675 680 685

Arg Thr Ile Gln Thr Tyr Glu Gln Ile Ile Ala Pro Ile Leu Lys Arg
 690 695 700

His Gly Asp Val Asp Ser Ser Gly Leu Ile Asn Trp Cys Ile Asp Glu
 705 710 715 720

Phe Thr Lys Leu Cys Lys Gln Ile Lys Lys His Leu Tyr Gly Thr Leu
 725 730 735

Leu Ile Ser Ser Gly Ile Asn Met Glu Thr Asp Glu Pro Ile Tyr Lys
 740 745 750

Val Lys Glu Arg Lys Leu Tyr Asp Asn Phe Leu Lys Ile Met Gln Pro
 755 760 765

Gln Leu Glu Glu Leu Lys Leu Val Gly Leu Asn Val Asp Tyr Ile Phe
 770 775 780

Glu Ser Ile Leu Asn Leu Glu
 785 790

<210> 7

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic probe

<400> 7

ctgcagtaaa ccctccagat ataacagact ctttatgtcc agtgatttcg ccaacaaatc 60

ttgggtggttg ggtgtgtgtg gtccataagt atgccgtgtt gtcaccaccc ccagtcaata 120

ccattggcaa tttaggatgt gaaaaaatag taaatatact atcggtatgt ttatcaaaat 180

aagtccatga attgttggac atgtcaattt ctaaagtctc atgtcatca tctaattcca 240

tctctcctc tctctcctc ggtggcgctt gatcatc tgcacttcc tcagccactt 300
 cattaacatt gatataattct tcttgagtat cgtctacgac gtc 343

<210> 8
 <211> 1248
 <212> DNA
 <213> Candida albicans

<220>
 <221> CDS
 <222> (1)..(1245)

<220>
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 <222> (1)..(1245)
 <223> gene CaIR012

<400> 8
 atg tca cac caa caa gaa gac gtc gta gac gat act caa gaa gaa tat 48
 Met Ser His Gln Gln Glu Asp Val Val Asp Asp Thr Gln Glu Glu Tyr
 1 5 10 15
 atc aat gtt aat gaa gtg gct gag gaa gtt gca gat gat gat caa gcg 96
 Ile Asn Val Asn Glu Val Ala Glu Glu Val Ala Asp Asp Asp Gln Ala
 20 25 30
 cca ccc gat gaa gaa gat gag gag atg gaa tta gat gat gag cat gag 144
 Pro Pro Asp Glu Glu Asp Glu Glu Met Glu Leu Asp Asp Glu His Glu
 35 40 45
 act tta gaa att gac atg tcc aac aat tca tgg act tat ttt gat aaa 192
 Thr Leu Glu Ile Asp Met Ser Asn Asn Ser Trp Thr Tyr Phe Asp Lys
 50 55 60
 cat acc gat agt ata ttt act att ttt tca cat cct aaa ttg cca atg 240
 His Thr Asp Ser Ile Phe Thr Ile Phe Ser His Pro Lys Leu Pro Met
 65 70 75 80
 gta ttg act ggg ggt ggt gac aac acg gca tac tta tgg acc aca cac 288
 Val Leu Thr Gly Gly Gly Asp Asn Thr Ala Tyr Leu Trp Thr Thr His
 85 90 95
 acc caa cca cca aga ttt gtt ggc gaa atc act gga cat aaa gag tct 336
 Thr Gln Pro Pro Arg Phe Val Gly Glu Ile Thr Gly His Lys Glu Ser
 100 105 110
 gtt ata tct gga ggg ttt act gca gac ggc aag ttt gtt gtt act gca 384
 Val Ile Ser Gly Gly Phe Thr Ala Asp Gly Lys Phe Val Val Thr Ala
 115 120 125

gac atg aat gga tta att caa gtt ttc aaa gcc aca aaa gga ggt gaa	432
Asp Met Asn Gly Leu Ile Gln Val Phe Lys Ala Thr Lys Gly Gly Glu	
130 135 140	
cag tgg gtg aaa ttt ggt gaa ttg gac gaa gtt gaa gaa gtg ttg ttt	480
Gln Trp Val Lys Phe Gly Glu Leu Asp Glu Val Glu Glu Val Leu Phe	
145 150 155 160	
gtt act gtg cat cca aca tta cca ttc ttt gcc ttt ggt gct acc gat	528
Val Thr Val His Pro Thr Leu Pro Phe Phe Ala Phe Gly Ala Thr Asp	
165 170 175	
gga tct ata tgg gtc tac caa ata gac gaa tcc agt aaa ctg cta gtg	576
Gly Ser Ile Trp Val Tyr Gln Ile Asp Glu Ser Ser Lys Leu Leu Val	
180 185 190	
caa att atg tct ggg ttc tca cac aca tta gaa tgt aat ggt gct gta	624
Gln Ile Met Ser Gly Phe Ser His Thr Leu Glu Cys Asn Gly Ala Val	
195 200 205	
ttt ata caa gga aaa gat gaa aat gat ttg aca ttg gtc tct ata agt	672
Phe Ile Gln Gly Lys Asp Glu Asn Asp Leu Thr Leu Val Ser Ile Ser	
210 215 220	
gaa gat ggt act gtg gtg aac tgg aac tgt ttt aca gga caa gtg aat	720
Glu Asp Gly Thr Val Val Asn Trp Asn Cys Phe Thr Gly Gln Val Asn	
225 230 235 240	
tat aaa ttg caa cct cat gat gac ttt aaa gga gtt gaa agt ccg tgg	768
Tyr Lys Leu Gln Pro His Asp Asp Phe Lys Gly Val Glu Ser Pro Trp	
245 250 255	
gtc acg gtc aaa gta cat ggt aat ctt gtg gcc att ggt ggc aga gat	816
Val Thr Val Lys Val His Gly Asn Leu Val Ala Ile Gly Gly Arg Asp	
260 265 270	
ggc cag cta tca att gtg aac aat gac act ggt aaa atc gtt cat act	864
Gly Gln Leu Ser Ile Val Asn Asn Asp Thr Gly Lys Ile Val His Thr	
275 280 285	
ctt aaa aca ttg gat aat gtc gac gac att gca gaa ctc tca att gag	912
Leu Lys Thr Leu Asp Asn Val Asp Asp Ile Ala Glu Leu Ser Ile Glu	
290 295 300	
gca ttg agt tgg tgt gaa agc aaa aat att aac ctc ttg gca gtg ggt	960
Ala Leu Ser Trp Cys Glu Ser Lys Asn Ile Asn Leu Leu Ala Val Gly	
305 310 315 320	
ttg gtt tct ggt gac gtt tta tta ttt gat act cag caa tgg aga ttg	1008
Leu Val Ser Gly Asp Val Leu Leu Phe Asp Thr Gln Gln Trp Arg Leu	
325 330 335	

aga aag aac ttg aaa gtt gac gat gcc atc acc aaa tta caa ttt gtt 1056
 Arg Lys Asn Leu Lys Val Asp Asp Ala Ile Thr Lys Leu Gln Phe Val
 340 345 350

ggc gaa acc ccc att ttg gtg gga agt agt atg gat ggt aaa att tac 1104
 Gly Glu Thr Pro Ile Leu Val Gly Ser Ser Met Asp Gly Lys Ile Tyr
 355 360 365

aaa tgg gac gct aga act ggt gaa gag ttg ttt gct ggt gtg gga cac 1152
 Lys Trp Asp Ala Arg Thr Gly Glu Glu Leu Phe Ala Gly Val Gly His
 370 375 380

aac atg gga gta ttg gac ttt gct att tta gat gga ggt aaa aag ttg 1200
 Asn Met Gly Val Leu Asp Phe Ala Ile Leu Asp Gly Gly Lys Lys Leu
 385 390 395 400

gtt act gct ggt gat gaa ggt gtt tca ttg gtc ttt gta cat gaa tag 1248
 Val Thr Ala Gly Asp Glu Gly Val Ser Leu Val Phe Val His Glu
 405 410 415

<210> 9

<211> 415

<212> PRT

<213> Candida albicans

<400> 9

Met Ser His Gln Gln Glu Asp Val Val Asp Asp Thr Gln Glu Glu Tyr
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Ile Asn Val Asn Glu Val Ala Glu Glu Val Ala Asp Asp Asp Gln Ala
 20 25 30

Pro Pro Asp Glu Glu Asp Glu Glu Met Glu Leu Asp Asp Glu His Glu
 35 40 45

Thr Leu Glu Ile Asp Met Ser Asn Asn Ser Trp Thr Tyr Phe Asp Lys
 50 55 60

His Thr Asp Ser Ile Phe Thr Ile Phe Ser His Pro Lys Leu Pro Met
 65 70 75 80

Val Leu Thr Gly Gly Gly Asp Asn Thr Ala Tyr Leu Trp Thr Thr His
 85 90 95

Thr Gln Pro Pro Arg Phe Val Gly Glu Ile Thr Gly His Lys Glu Ser
 100 105 110

Val Ile Ser Gly Gly Phe Thr Ala Asp Gly Lys Phe Val Val Thr Ala
 115 120 125

Asp Met Asn Gly Leu Ile Gln Val Phe Lys Ala Thr Lys Gly Gly Glu
 130 135 140

Gln	Trp	Val	Lys	Phe	Gly	Glu	Leu	Asp	Glu	Val	Glu	Glu	Val	Leu	Phe	145	150	155	160
Val	Thr	Val	His	Pro	Thr	Leu	Pro	Phe	Phe	Ala	Phe	Gly	Ala	Thr	Asp	165	170	175	
Gly	Ser	Ile	Trp	Val	Tyr	Gln	Ile	Asp	Glu	Ser	Ser	Lys	Leu	Leu	Val	180	185	190	
Gln	Ile	Met	Ser	Gly	Phe	Ser	His	Thr	Leu	Glu	Cys	Asn	Gly	Ala	Val	195	200	205	
Phe	Ile	Gln	Gly	Lys	Asp	Glu	Asn	Asp	Leu	Thr	Leu	Val	Ser	Ile	Ser	210	215	220	
Glu	Asp	Gly	Thr	Val	Val	Asn	Trp	Asn	Cys	Phe	Thr	Gly	Gln	Val	Asn	225	230	235	240
Tyr	Lys	Leu	Gln	Pro	His	Asp	Asp	Phe	Lys	Gly	Val	Glu	Ser	Pro	Trp	245	250	255	
Val	Thr	Val	Lys	Val	His	Gly	Asn	Leu	Val	Ala	Ile	Gly	Gly	Arg	Asp	260	265	270	
Gly	Gln	Leu	Ser	Ile	Val	Asn	Asn	Asp	Thr	Gly	Lys	Ile	Val	His	Thr	275	280	285	
Leu	Lys	Thr	Leu	Asp	Asn	Val	Asp	Asp	Ile	Ala	Glu	Leu	Ser	Ile	Glu	290	295	300	
Ala	Leu	Ser	Trp	Cys	Glu	Ser	Lys	Asn	Ile	Asn	Leu	Leu	Ala	Val	Gly	305	310	315	320
Leu	Val	Ser	Gly	Asp	Val	Leu	Leu	Phe	Asp	Thr	Gln	Gln	Trp	Arg	Leu	325	330	335	
Arg	Lys	Asn	Leu	Lys	Val	Asp	Asp	Ala	Ile	Thr	Lys	Leu	Gln	Phe	Val	340	345	350	
Gly	Glu	Thr	Pro	Ile	Leu	Val	Gly	Ser	Ser	Met	Asp	Gly	Lys	Ile	Tyr	355	360	365	
Lys	Trp	Asp	Ala	Arg	Thr	Gly	Glu	Glu	Leu	Phe	Ala	Gly	Val	Gly	His	370	375	380	
Asn	Met	Gly	Val	Leu	Asp	Phe	Ala	Ile	Leu	Asp	Gly	Gly	Lys	Lys	Leu	385	390	395	400
Val	Thr	Ala	Gly	Asp	Glu	Gly	Val	Ser	Leu	Val	Phe	Val	His	Glu		405	410	415	

<210> 10
 <211> 5544
 <212> DNA
 <213> *Candida albicans*

<220>
 <221> CDS
 <222> (1) .. (5541)

<220>
 <221> gene
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 <223> gene CaJL039

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 1 5 10 15

aac acc ctc aag ttt gag tcc aat ata gat ttg gat aca atc gac ttc 96
 Asn Thr Leu Lys Phe Glu Ser Asn Ile Asp Leu Asp Thr Ile Asp Phe
 20 25 30

acc agc atc aag aat gat ctt gca aat gtt ttg att aca cca gtc cct 144
 Thr Ser Ile Lys Asn Asp Leu Ala Asn Val Leu Ile Thr Pro Val Pro
 35 40 45

ctg gat caa tca cgt agc aaa ctt gga gac gca tca aaa cca gtg gcg 192
 Leu Asp Gln Ser Arg Ser Lys Leu Gly Asp Ala Ser Lys Pro Val Ala
 50 55 60

ttg ccc agt gga gat gag gtg aaa ttg aat caa gca tca att gaa att 240
 Leu Pro Ser Gly Asp Glu Val Lys Leu Asn Gln Ala Ser Ile Glu Ile
 65 70 75 80

act gga gtt tta tca aat gaa ttg gat tta gat gaa cta aat aca gca 288
 Thr Gly Val Leu Ser Asn Glu Leu Asp Leu Asp Glu Leu Asn Thr Ala
 85 90 95

gag ttg tta tat aac gca agt gac ttg agc tac aag aag gga acg tcc 336
 Glu Leu Leu Tyr Asn Ala Ser Asp Leu Ser Tyr Lys Lys Gly Thr Ser
 100 105 110

att ggc gat agt gct cga ttg gct tat tat tta aga gct cat tat ata 384
 Ile Gly Asp Ser Ala Arg Leu Ala Tyr Tyr Leu Arg Ala His Tyr Ile
 115 120 125

cta aac att gtt gga tac tta gtt tgc cat aaa cgt tta gat atc atc 432
 Leu Asn Ile Val Gly Tyr Leu Val Ser His Lys Arg Leu Asp Ile Ile
 130 135 140

act aac aac aac caa gtg ttg ttt gac aat att ttg aaa agt ttc agc 480
 Thr Asn Asn Asn Gln Val Leu Phe Asp Asn Ile Leu Lys Ser Phe Ser
 145 150 155 160

aag att tat act ttg agt ggt aaa tta aat gac atg att gac aag caa	528
Lys Ile Tyr Thr Leu Ser Gly Lys Leu Asn Asp Met Ile Asp Lys Gln	
165 170 175	
aaa gtt acc ggc gac atc aac aat ctt gca ttt atc aat tgt atc aat	576
Lys Val Thr Gly Asp Ile Asn Asn Leu Ala Phe Ile Asn Cys Ile Asn	
180 185 190	
tat tcc aga agt cag ttg ttt aat gca cac gag tta ttg gga caa gtt	624
Tyr Ser Arg Ser Gln Leu Phe Asn Ala His Glu Leu Leu Gly Gln Val	
195 200 205	
gta ttt gga tta gcg gat aat tat tat gag agt tat ggc aca cta aac	672
Val Phe Gly Leu Ala Asp Asn Tyr Tyr Glu Ser Tyr Gly Thr Leu Asn	
210 215 220	
aac tat aat tcc tta gtg gag ttt ata ctg aaa aat atc agc gat gaa	720
Asn Tyr Asn Ser Leu Val Glu Phe Ile Leu Lys Asn Ile Ser Asp Glu	
225 230 235 240	
gat gtt ttt gtt atc cat ttt tta cca tcc act tta caa ttg ttc aag	768
Asp Val Phe Val Ile His Phe Leu Pro Ser Thr Leu Gln Leu Phe Lys	
245 250 255	
aaa tta ctt caa cta ggt gag gaa tct tta gtc gat cag ttt tac aag	816
Lys Leu Leu Gln Leu Gly Glu Glu Ser Leu Val Asp Gln Phe Tyr Lys	
260 265 270	
act ata acc tct tcc ata cta aaa gat tat gaa gcc aac aat ttt tcc	864
Thr Ile Thr Ser Ser Ile Leu Lys Asp Tyr Glu Ala Asn Asn Phe Ser	
275 280 285	
aaa agt gaa gat att gac ttg tca aaa tca aaa ttg tct ggc ttt gaa	912
Lys Ser Glu Asp Ile Asp Leu Ser Lys Ser Lys Leu Ser Gly Phe Glu	
290 295 300	
ata gtc aca agc ttt att ttt cta act gag ttt att cca tgg tgc aag	960
Ile Val Thr Ser Phe Ile Phe Leu Thr Glu Phe Ile Pro Trp Cys Lys	
305 310 315 320	
cag ctg tca agt aga acc gcg aaa tac gat ttc aaa gat gat ata tta	1008
Gln Leu Ser Ser Arg Thr Ala Lys Tyr Asp Phe Lys Asp Asp Ile Leu	
325 330 335	
aag tat atg gaa ttc ttg ata agt tat gga gtt atg gaa cga tta tta	1056
Lys Tyr Met Glu Phe Leu Ile Ser Tyr Gly Val Met Glu Arg Leu Leu	
340 345 350	
tca tac tgt tct gaa acc agc aat gca aaa act cag caa gtg tac gac	1104
Ser Tyr Cys Ser Glu Thr Ser Asn Ala Lys Thr Gln Gln Val Tyr Asp	
355 360 365	

tgg tca aac atg tac gat ttc aga gca ttg ctt caa aag aat ttc cca	1152
Trp Ser Asn Met Tyr Asp Phe Arg Ala Leu Leu Gln Lys Asn Phe Pro	
370 375 380	
cga ctt aca cca gca aaa ttt cat tat cct ggc aat caa gaa ttg ttg	1200
Arg Leu Thr Pro Ala Lys Phe His Tyr Pro Gly Asn Gln Glu Leu Leu	
385 390 395 400	
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Asn Ala Val Arg Pro Gly Tyr Glu Asn Ile Ser Lys Leu Ile Asp Ile	
405 410 415	
tcc ttt ttg acg tta gat cca tcg ctt aat gag acg ttg gtt tca cct	1296
Ser Phe Leu Thr Leu Asp Pro Ser Leu Asn Glu Thr Leu Val Ser Pro	
420 425 430	
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Phe Phe Gln Ser Phe Phe Ser Val Phe Ile Ser Asn Ala Ala Val Val	
435 440 445	
atg acc tct tta agg gac tca gag gaa gat ttt gtt tta tcg tcg ttg	1392
Met Thr Ser Leu Arg Asp Ser Glu Glu Asp Phe Val Leu Ser Ser Leu	
450 455 460	
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Asn Glu Ser Asp Glu Glu Glu Glu Glu Glu Glu Ser Asp Ser Asp Glu	
465 470 475 480	
gat tct tcg acc cca aaa aac aaa gaa aaa tca gct ggg tta gac ctt	1488
Asp Ser Ser Thr Pro Lys Asn Lys Glu Lys Ser Ala Gly Leu Asp Leu	
485 490 495	
gac aag att gcc cag cgt gct gaa tta gaa agg ttc tac ttg gct ttc	1536
Asp Lys Ile Ala Gln Arg Ala Glu Leu Glu Arg Phe Tyr Leu Ala Phe	
500 505 510	
gcg tac acc tac aac aat cga cct gaa ttg tgt gcg tta ttt tgg ggg	1584
Ala Tyr Thr Tyr Asn Asn Arg Pro Glu Leu Cys Ala Leu Phe Trp Gly	
515 520 525	
aac gag cag gta act cat gac att ata gga ttt att tcc tgg gga ctt	1632
Asn Glu Gln Val Thr His Asp Ile Ile Gly Phe Ile Ser Trp Gly Leu	
530 535 540	
gct aat aat acg tct ccg ttg atc act gca aca ttc tgc tta cta tta	1680
Ala Asn Asn Thr Ser Pro Leu Ile Thr Ala Thr Phe Cys Leu Leu Leu	
545 550 555 560	
ggg tcg ttg gca tct gct ggt gca gag gca act tca agg ata tgg gag	1728
Gly Ser Leu Ala Ser Ala Gly Ala Glu Ala Thr Ser Arg Ile Trp Glu	
565 570 575	

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Ile Leu Val His Asn Asn Asn Asn Ala Ser Thr Arg Lys Asn Asp Phe	
580 585 590	
tca aag gta tcc gtt gac tcc ctt tat gat tct ttg aaa tat tac att	1824
Ser Lys Val Ser Val Asp Ser Leu Tyr Asp Ser Leu Lys Tyr Tyr Ile	
595 600 605	
gac tct tta aat gaa agc ttt gaa caa gat tta aat gcc caa ttg atg	1872
Asp Ser Leu Asn Glu Ser Phe Glu Gln Asp Leu Asn Ala Gln Leu Met	
610 615 620	
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Leu Asn Gln Lys Lys Gln Asp Phe Leu Phe Ser Thr Thr Thr Ser Lys	
625 630 635 640	
cag gac ctt gat gat tct ggc gag aat aga att gtt ata gag ttg gcc	1968
Gln Asp Leu Asp Asp Ser Gly Glu Asn Arg Ile Val Ile Glu Leu Ala	
645 650 655	
gag gat tca ctt gtc ctc att tca ggg ttt att caa tta ctt tct gca	2016
Glu Asp Ser Leu Val Leu Ile Ser Gly Phe Ile Gln Leu Leu Ser Ala	
660 665 670	
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Ile Val Lys Asn Leu Asn Thr Lys Asn Glu Arg Ser Lys Glu Ile Lys	
675 680 685	
tcc gtg gta tac act aga ttc tca cca atc att aaa ggg ttt tta aaa	2112
Ser Val Val Tyr Thr Arg Phe Ser Pro Ile Ile Lys Gly Phe Leu Lys	
690 695 700	
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Phe Asp Asn Leu Ile Asn Gly Ser Arg Phe Leu Gln Val Asp Ala Ser	
705 710 715 720	
att caa agc aca aac aac ccc aaa ttt att gat ttg cca aat gtt ttc	2208
Ile Gln Ser Thr Asn Asn Pro Lys Phe Ile Asp Leu Pro Asn Val Phe	
725 730 735	
gtc agt gat gac tct aga att ata ttg acg aac ctc att cta acc ttt	2256
Val Ser Asp Asp Ser Arg Ile Ile Leu Thr Asn Leu Ile Leu Thr Phe	
740 745 750	
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Leu Gly Asp Phe Val Thr Asn Asp Ser Asp Pro Tyr Ile Arg Tyr Glu	
755 760 765	
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Ile Trp Arg Leu Val Asp Arg Trp Met Tyr Gln Gly Leu His Ser Leu	
770 775 780	

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Pro Glu Asp Lys Lys Asp Asp Ala Phe Arg His Ile Lys Arg Lys Tyr	
785 790 795 800	
aac agt aag aaa aat gtt ccc atc aat caa gca ttt tca aca aac cta	2448
Asn Ser Lys Lys Asn Val Pro Ile Asn Gln Ala Phe Ser Thr Asn Leu	
805 810 815	
act cat ctt agt caa att ggg aat ttc act gtc ttg gtg aaa aaa ttg	2496
Thr His Leu Ser Gln Ile Gly Asn Phe Thr Val Leu Val Lys Lys Leu	
820 825 830	
tta acc cca tat gca gat agt aat gaa gca ttc acc aag tac tcg ttg	2544
Leu Thr Pro Tyr Ala Asp Ser Asn Glu Ala Phe Thr Lys Tyr Ser Leu	
835 840 845	
ttg tat cct tgt gac tta gga tta ggg tat aga ttc aac aac caa ctt	2592
Leu Tyr Pro Cys Asp Leu Gly Leu Gly Tyr Arg Phe Asn Asn Gln Leu	
850 855 860	
gga att tgg cca tac att gaa ttt tta atg caa aat gtg ttt gca aat	2640
Gly Ile Trp Pro Tyr Ile Glu Phe Leu Met Gln Asn Val Phe Ala Asn	
865 870 875 880	
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Ser Gly Thr Ile Ala Asn Lys Arg Asp Arg Val Asn Leu Gln Leu Asn	
885 890 895	
ttg cta gaa tta ttt agc aat gca tta cag gga gtt gac tgg aag ttt	2736
Leu Leu Glu Leu Phe Ser Asn Ala Leu Gln Gly Val Asp Trp Lys Phe	
900 905 910	
ctt att gat gtg gca ccg aaa att att cgt gac ttg aaa aat ttt aat	2784
Leu Ile Asp Val Ala Pro Lys Ile Ile Arg Asp Leu Lys Asn Phe Asn	
915 920 925	
ggg ata ttt gac tcg ctt att cct ggt gtt caa ttg gac ttt gaa gtg	2832
Gly Ile Phe Asp Ser Leu Ile Pro Gly Val Gln Leu Asp Phe Glu Val	
930 935 940	
ttt gtc aaa ttg cat cat tca gtt gct gtg att aac tat cta ttt gaa	2880
Phe Val Lys Leu His His Ser Val Ala Val Ile Asn Tyr Leu Phe Glu	
945 950 955 960	
aac agg aca ttt tct gcc ttg ttt aag ctt gtt aat att gga gtt gat	2928
Asn Arg Thr Phe Ser Ala Leu Phe Lys Leu Val Asn Ile Gly Val Asp	
965 970 975	
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Ser Val Asn Glu Ser Gly Glu Ser Ala Glu Leu Val Ser His Ala Leu	
980 985 990	

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cct aga acc ata ttt gat tgt ata tac tat cca aag aat ttg gga aca Pro Arg Thr Ile Phe Asp Cys Ile Tyr Tyr Pro Lys Asn Leu Gly Thr 1045 1050 1055	3168
cat ggt gtt gct gat ttt tac gaa gtg ata ttg ttc cac tta tct gca His Gly Val Ala Asp Phe Tyr Glu Val Ile Leu Phe His Leu Ser Ala 1060 1065 1070	3216
gtt gtc caa ttt gcc ctt tat gtc agt tgt gaa aat act att tcc aac Val Val Gln Phe Ala Leu Tyr Val Ser Cys Glu Asn Thr Ile Ser Asn 1075 1080 1085	3264
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acc aga gtt tca agc tct gct gat ccc tta ctc aac aac gat aga ttg Thr Arg Val Ser Ser Ala Asp Pro Leu Leu Asn Asn Asp Arg Leu 1105 1110 1115 1120	3360
att acc aca ttt gaa aac atc gac gag tca ata aaa atc aag ttt gct Ile Thr Thr Phe Glu Asn Ile Asp Glu Ser Ile Lys Ile Lys Phe Ala 1125 1130 1135	3408
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gag ata ttg gat ttt gtt ttg ggc aat ctc aat caa ttt gat ggc aaa Glu Ile Leu Asp Phe Val Leu Gly Asn Leu Asn Gln Phe Asp Gly Lys 1155 1160 1165	3504
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Phe Leu Asn Thr Leu Ser Ile Ser Leu Asp Leu Ile Ser Glu Ile Asp	
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Tyr Asn Asn Gly Asn Asn His Ile Ile Asp Val Gly Pro Ala Lys Leu	
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Ser Ser Leu Ile Leu Gln Ile Leu Ile Lys Leu Cys Gln Asp Pro Ile	
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Ser Ser Ser Ile Thr Leu Asn Gln Leu Arg Glu Tyr Glu Glu Leu Phe	
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1265 1270 1275 1280	
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Cys Gly Asn Gln Phe Asp Gly Asp Leu Gln Ile Asp Ala Ser Asn Val	
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Gln Arg Asn Leu Ile Leu Gln Tyr Leu Ser Leu Glu Phe His Ser Val	
1315 1320 1325	
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Lys Ser Arg Thr Lys Arg Glu Tyr Tyr Ser Lys Val Leu Thr Asn Asp	
1330 1335 1340	
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Lys Glu Phe Val Asn Arg Thr Pro Lys Val Leu Thr Phe Leu Asn Ile	
1345 1350 1355 1360	
cta aat tat tca ttc aag aac ttt gaa gtg cag aaa tac gaa tgg ctt	4128
Leu Asn Tyr Ser Phe Lys Asn Phe Glu Val Gln Lys Tyr Glu Trp Leu	
1365 1370 1375	
gac caa aaa ttt aac gtg tcg ttg tta ttg gca gaa gta aac gct caa	4176
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1380 1385 1390	
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Lys Asn Gly Thr Leu Asp Phe Ser Val Leu Thr Lys Val Phe Arg Leu	
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Ala Glu Glu Ile Met Val Glu Gly Ser Lys Ile Ser Asp Phe Val Thr	
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Lys Tyr Leu Val Ser Thr Asp Leu Lys Asp Val Gln Leu Lys Cys Leu	
1445 1450 1455	
cat tca tgg tgt caa ttg ata gag att ttg gtt act gac agt gga atc	4416
His Ser Trp Cys Gln Leu Ile Glu Ile Leu Val Thr Asp Ser Gly Ile	
1460 1465 1470	
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Asn Ser Leu Asn Phe Ile Leu Glu Val Leu Gln Val Ile Ile Pro Lys	
1475 1480 1485	
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Ile Asn Asp Tyr Phe Asp Val Asp Ile Leu Phe Ser Glu Glu Met Val	
1490 1495 1500	
tca tta tgt gtt tta ttg ttt gat ctt tat gat cag ctg act ctt gcg	4560
Ser Leu Cys Val Leu Leu Phe Asp Leu Tyr Asp Gln Leu Thr Leu Ala	
1505 1510 1515 1520	
gac aga aaa ggt gaa gat ttt gca ctt gga att gag aga ttg atc ccc	4608
Asp Arg Lys Gly Glu Asp Phe Ala Leu Gly Ile Glu Arg Leu Ile Pro	
1525 1530 1535	
tta ttt cag act tgt att gca ggt att ctt aat tct aac tca aca ccc	4656
Leu Phe Gln Thr Cys Ile Ala Gly Ile Leu Asn Ser Asn Ser Thr Pro	
1540 1545 1550	
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Ser Leu Arg Ser Asp Leu Tyr Val Val Gly Asn Lys Phe Leu Leu Lys	
1555 1560 1565	
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Cys Phe Glu Arg Glu Ser Phe Leu Lys Gln Val Met His Ile Ile Lys	
1570 1575 1580	
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aat gaa ttg ttt tca att ttg cat cag tcg aag ttt ttg cag att gat Asn Glu Leu Phe Ser Ile Leu His Gln Ser Lys Phe Leu Gln Ile Asp 1700 1705 1710	5136
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act gtc aat gta aat gtt ttg cta gat act cca ctt tcg ata act gac Thr Val Asn Val Asn Val Leu Leu Asp Thr Pro Leu Ser Ile Thr Asp 1730 1735 1740	5232
ttg gtg gat cca tac aag ttg cga agt gaa aac act ata tca tat ttt Leu Val Asp Pro Tyr Lys Leu Arg Ser Glu Asn Thr Ile Ser Tyr Phe 1745 1750 1755 1760	5280
gag ttc ctt gta cca ata ttt cag cta ctt aca aca gtg tta ttg tca Glu Phe Leu Val Pro Ile Phe Gln Leu Leu Thr Thr Val Leu Leu Ser 1765 1770 1775	5328
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gta gag acc aaa caa att ggt caa ggg ttg tac aag gaa gag agt cac Val Glu Thr Lys Gln Ile Gly Gln Gly Leu Tyr Lys Glu Glu Ser His 1810 1815 1820	5472

gag ttg gta tcg ttg aaa gaa ttg gtg aag ttg ttt att ttg att gat 5520
 Glu Leu Val Ser Leu Lys Glu Leu Val Lys Leu Phe Ile Leu Ile Asp
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 Ser Leu Ala His Tyr Ser Val
 1845

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 Thr Ser Ile Lys Asn Asp Leu Ala Asn Val Leu Ile Thr Pro Val Pro
 35 40 45
 Leu Asp Gln Ser Arg Ser Lys Leu Gly Asp Ala Ser Lys Pro Val Ala
 50 55 60
 Leu Pro Ser Gly Asp Glu Val Lys Leu Asn Gln Ala Ser Ile Glu Ile
 65 70 75 80
 Thr Gly Val Leu Ser Asn Glu Leu Asp Leu Asp Glu Leu Asn Thr Ala
 85 90 95
 Glu Leu Leu Tyr Asn Ala Ser Asp Leu Ser Tyr Lys Lys Gly Thr Ser
 100 105 110
 Ile Gly Asp Ser Ala Arg Leu Ala Tyr Tyr Leu Arg Ala His Tyr Ile
 115 120 125
 Leu Asn Ile Val Gly Tyr Leu Val Ser His Lys Arg Leu Asp Ile Ile
 130 135 140
 Thr Asn Asn Asn Gln Val Leu Phe Asp Asn Ile Leu Lys Ser Phe Ser
 145 150 155 160
 Lys Ile Tyr Thr Leu Ser Gly Lys Leu Asn Asp Met Ile Asp Lys Gln
 165 170 175
 Lys Val Thr Gly Asp Ile Asn Asn Leu Ala Phe Ile Asn Cys Ile Asn
 180 185 190
 Tyr Ser Arg Ser Gln Leu Phe Asn Ala His Glu Leu Leu Gly Gln Val
 195 200 205

Val	Phe	Gly	Leu	Ala	Asp	Asn	Tyr	Tyr	Glu	Ser	Tyr	Gly	Thr	Leu	Asn	210	215	220
Asn	Tyr	Asn	Ser	Leu	Val	Glu	Phe	Ile	Leu	Lys	Asn	Ile	Ser	Asp	Glu	225	230	235
Asp	Val	Phe	Val	Ile	His	Phe	Leu	Pro	Ser	Thr	Leu	Gln	Leu	Phe	Lys	245	250	255
Lys	Leu	Leu	Gln	Leu	Gly	Glu	Glu	Ser	Leu	Val	Asp	Gln	Phe	Tyr	Lys	260	265	270
Thr	Ile	Thr	Ser	Ser	Ile	Leu	Lys	Asp	Tyr	Glu	Ala	Asn	Asn	Phe	Ser	275	280	285
Lys	Ser	Glu	Asp	Ile	Asp	Leu	Ser	Lys	Ser	Lys	Leu	Ser	Gly	Phe	Glu	290	295	300
Ile	Val	Thr	Ser	Phe	Ile	Phe	Leu	Thr	Glu	Phe	Ile	Pro	Trp	Cys	Lys	305	310	315
Gln	Leu	Ser	Ser	Arg	Thr	Ala	Lys	Tyr	Asp	Phe	Lys	Asp	Asp	Ile	Leu	325	330	335
Lys	Tyr	Met	Glu	Phe	Leu	Ile	Ser	Tyr	Gly	Val	Met	Glu	Arg	Leu	Leu	340	345	350
Ser	Tyr	Cys	Ser	Glu	Thr	Ser	Asn	Ala	Lys	Thr	Gln	Gln	Val	Tyr	Asp	355	360	365
Trp	Ser	Asn	Met	Tyr	Asp	Phe	Arg	Ala	Leu	Leu	Gln	Lys	Asn	Phe	Pro	370	375	380
Arg	Leu	Thr	Pro	Ala	Lys	Phe	His	Tyr	Pro	Gly	Asn	Gln	Glu	Leu	Leu	385	390	395
Asn	Ala	Val	Arg	Pro	Gly	Tyr	Glu	Asn	Ile	Ser	Lys	Leu	Ile	Asp	Ile	405	410	415
Ser	Phe	Leu	Thr	Leu	Asp	Pro	Ser	Leu	Asn	Glu	Thr	Leu	Val	Ser	Pro	420	425	430
Phe	Phe	Gln	Ser	Phe	Phe	Ser	Val	Phe	Ile	Ser	Asn	Ala	Ala	Val	Val	435	440	445
Met	Thr	Ser	Leu	Arg	Asp	Ser	Glu	Glu	Asp	Phe	Val	Leu	Ser	Ser	Leu	450	455	460
Asn	Glu	Ser	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Ser	Asp	Ser	Asp	Glu	465	470	475
Asp	Ser	Ser	Thr	Pro	Lys	Asn	Lys	Glu	Lys	Ser	Ala	Gly	Leu	Asp	Leu	485	490	495

Asp	Lys	Ile	Ala	Gln	Arg	Ala	Glu	Leu	Glu	Arg	Phe	Tyr	Leu	Ala	Phe	500	505	510
Ala	Tyr	Thr	Tyr	Asn	Asn	Arg	Pro	Glu	Leu	Cys	Ala	Leu	Phe	Trp	Gly	515	520	525
Asn	Glu	Gln	Val	Thr	His	Asp	Ile	Ile	Gly	Phe	Ile	Ser	Trp	Gly	Leu	530	535	540
Ala	Asn	Asn	Thr	Ser	Pro	Leu	Ile	Thr	Ala	Thr	Phe	Cys	Leu	Leu	Leu	545	550	555
Gly	Ser	Leu	Ala	Ser	Ala	Gly	Ala	Glu	Ala	Thr	Ser	Arg	Ile	Trp	Glu	565	570	575
Ile	Leu	Val	His	Asn	Asn	Asn	Asn	Ala	Ser	Thr	Arg	Lys	Asn	Asp	Phe	580	585	590
Ser	Lys	Val	Ser	Val	Asp	Ser	Leu	Tyr	Asp	Ser	Leu	Lys	Tyr	Tyr	Ile	595	600	605
Asp	Ser	Leu	Asn	Glu	Ser	Phe	Glu	Gln	Asp	Leu	Asn	Ala	Gln	Leu	Met	610	615	620
Leu	Asn	Gln	Lys	Lys	Gln	Asp	Phe	Leu	Phe	Ser	Thr	Thr	Thr	Ser	Lys	625	630	635
Gln	Asp	Leu	Asp	Asp	Ser	Gly	Glu	Asn	Arg	Ile	Val	Ile	Glu	Leu	Ala	645	650	655
Glu	Asp	Ser	Leu	Val	Leu	Ile	Ser	Gly	Phe	Ile	Gln	Leu	Leu	Ser	Ala	660	665	670
Ile	Val	Lys	Asn	Leu	Asn	Thr	Lys	Asn	Glu	Arg	Ser	Lys	Glu	Ile	Lys	675	680	685
Ser	Val	Val	Tyr	Thr	Arg	Phe	Ser	Pro	Ile	Ile	Lys	Gly	Phe	Leu	Lys	690	695	700
Phe	Asp	Asn	Leu	Ile	Asn	Gly	Ser	Arg	Phe	Leu	Gln	Val	Asp	Ala	Ser	705	710	715
Ile	Gln	Ser	Thr	Asn	Asn	Pro	Lys	Phe	Ile	Asp	Leu	Pro	Asn	Val	Phe	725	730	735
Val	Ser	Asp	Asp	Ser	Arg	Ile	Ile	Leu	Thr	Asn	Leu	Ile	Leu	Thr	Phe	740	745	750
Leu	Gly	Asp	Phe	Val	Thr	Asn	Asp	Ser	Asp	Pro	Tyr	Ile	Arg	Tyr	Glu	755	760	765
Ile	Trp	Arg	Leu	Val	Asp	Arg	Trp	Met	Tyr	Gln	Gly	Leu	His	Ser	Leu	770	775	780

Pro	Glu	Asp	Lys	Lys	Asp	Asp	Ala	Phe	Arg	His	Ile	Lys	Arg	Lys	Tyr	
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Asn	Ser	Lys	Lys	Asn	Val	Pro	Ile	Asn	Gln	Ala	Phe	Ser	Thr	Asn	Leu	
				805					810					815		
Thr	His	Leu	Ser	Gln	Ile	Gly	Asn	Phe	Thr	Val	Leu	Val	Lys	Lys	Leu	
			820					825					830			
Leu	Thr	Pro	Tyr	Ala	Asp	Ser	Asn	Glu	Ala	Phe	Thr	Lys	Tyr	Ser	Leu	
		835					840					845				
Leu	Tyr	Pro	Cys	Asp	Leu	Gly	Leu	Gly	Tyr	Arg	Phe	Asn	Asn	Gln	Leu	
	850					855					860					
Gly	Ile	Trp	Pro	Tyr	Ile	Glu	Phe	Leu	Met	Gln	Asn	Val	Phe	Ala	Asn	
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Ser	Gly	Thr	Ile	Ala	Asn	Lys	Arg	Asp	Arg	Val	Asn	Leu	Gln	Leu	Asn	
				885					890					895		
Leu	Leu	Glu	Leu	Phe	Ser	Asn	Ala	Leu	Gln	Gly	Val	Asp	Trp	Lys	Phe	
		900						905					910			
Leu	Ile	Asp	Val	Ala	Pro	Lys	Ile	Ile	Arg	Asp	Leu	Lys	Asn	Phe	Asn	
		915						920				925				
Gly	Ile	Phe	Asp	Ser	Leu	Ile	Pro	Gly	Val	Gln	Leu	Asp	Phe	Glu	Val	
	930					935					940					
Phe	Val	Lys	Leu	His	His	Ser	Val	Ala	Val	Ile	Asn	Tyr	Leu	Phe	Glu	
945					950					955					960	
Asn	Arg	Thr	Phe	Ser	Ala	Leu	Phe	Lys	Leu	Val	Asn	Ile	Gly	Val	Asp	
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Ser	Val	Asn	Glu	Ser	Gly	Glu	Ser	Ala	Glu	Leu	Val	Ser	His	Ala	Leu	
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Gly	Leu	Ile	Asn	Ser	Leu	Leu	Arg	Val	Gln	Asn	Ser	Phe	Ile	Asn	Lys	
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Gly	Thr	Ala	Ile	Gly	Ile	Gly	Thr	Ser	Met	Ser	Leu	Ala	Leu	Ala	Thr	
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Pro	Arg	Thr	Ile	Phe	Asp	Cys	Ile	Tyr	Tyr	Pro	Lys	Asn	Leu	Gly	Thr	
				1045					1050					1055		
His	Gly	Val	Ala	Asp	Phe	Tyr	Glu	Val	Ile	Leu	Phe	His	Leu	Ser	Ala	
		1060					1065					1070				

Val	Val	Gln	Phe	Ala	Leu	Tyr	Val	Ser	Cys	Glu	Asn	Thr	Ile	Ser	Asn	
	1075						1080					1085				
Lys	Ala	Ile	Ser	Ile	Leu	Lys	Gly	Val	Ser	Gln	Ser	Lys	Phe	Phe	Val	
	1090					1095					1100					
Thr	Arg	Val	Ser	Ser	Ser	Ala	Asp	Pro	Leu	Leu	Asn	Asn	Asp	Arg	Leu	
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Ile	Thr	Thr	Phe	Glu	Asn	Ile	Asp	Glu	Ser	Ile	Lys	Ile	Lys	Phe	Ala	
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Phe	Ile	Asp	Lys	Phe	Glu	Glu	Leu	Glu	Asp	Ser	Leu	Asn	Met	Lys	Tyr	
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Glu	Ile	Leu	Asp	Phe	Val	Leu	Gly	Asn	Leu	Asn	Gln	Phe	Asp	Gly	Lys	
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Val	Ala	Thr	Thr	Ala	His	Phe	Leu	Leu	Gly	Tyr	Lys	Val	Lys	Gly	Asp	
	1170					1175					1180					
Thr	Leu	Asp	Leu	Val	Gln	Thr	Asn	Asp	Gln	Asn	Thr	Leu	Leu	Lys	Ser	
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Phe	Leu	Asn	Thr	Leu	Ser	Ile	Ser	Leu	Asp	Leu	Ile	Ser	Glu	Ile	Asp	
			1205						1210					1215		
Tyr	Asn	Asn	Gly	Asn	Asn	His	Ile	Ile	Asp	Val	Gly	Pro	Ala	Lys	Leu	
		1220						1225					1230			
Ser	Ser	Leu	Ile	Leu	Gln	Ile	Leu	Ile	Lys	Leu	Cys	Gln	Asp	Pro	Ile	
		1235					1240					1245				
Ser	Ser	Ser	Ile	Thr	Leu	Asn	Gln	Leu	Arg	Glu	Tyr	Glu	Glu	Leu	Phe	
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Glu	Lys	Leu	Val	Asn	Cys	Gln	Pro	Lys	Leu	Asp	Leu	Asn	Thr	Val	Trp	
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Cys	Gly	Asn	Gln	Phe	Asp	Gly	Asp	Leu	Gln	Ile	Asp	Ala	Ser	Asn	Val	
			1285						1290					1295		
Phe	Val	Asp	Asn	Gln	Ala	Ser	Thr	Gln	Ala	Phe	Phe	Ser	Phe	Ile	Asn	
		1300						1305					1310			
Gln	Arg	Asn	Leu	Ile	Leu	Gln	Tyr	Leu	Ser	Leu	Glu	Phe	His	Ser	Val	
	1315						1320					1325				
Lys	Ser	Arg	Thr	Lys	Arg	Glu	Tyr	Tyr	Ser	Lys	Val	Leu	Thr	Asn	Asp	
	1330					1335					1340					
Lys	Glu	Phe	Val	Asn	Arg	Thr	Pro	Lys	Val	Leu	Thr	Phe	Leu	Asn	Ile	
1345					1350					1355					1360	

Leu Asn Tyr Ser Phe Lys Asn Phe Glu Val Gln Lys Tyr Glu Trp Leu
 1365 1370 1375
 Asp Gln Lys Phe Asn Val Ser Leu Leu Leu Ala Glu Val Asn Ala Gln
 1380 1385 1390
 Lys Asn Gly Thr Leu Asp Phe Ser Val Leu Thr Lys Val Phe Arg Leu
 1395 1400 1405
 Leu Cys Gln Thr Ser Asn Leu Ile Thr Pro Glu Ser Lys Gln Leu Phe
 1410 1415 1420
 Ala Glu Glu Ile Met Val Glu Gly Ser Lys Ile Ser Asp Phe Val Thr
 1425 1430 1435 1440
 Lys Tyr Leu Val Ser Thr Asp Leu Lys Asp Val Gln Leu Lys Cys Leu
 1445 1450 1455
 His Ser Trp Cys Gln Leu Ile Glu Ile Leu Val Thr Asp Ser Gly Ile
 1460 1465 1470
 Asn Ser Leu Asn Phe Ile Leu Glu Val Leu Gln Val Ile Ile Pro Lys
 1475 1480 1485
 Ile Asn Asp Tyr Phe Asp Val Asp Ile Leu Phe Ser Glu Glu Met Val
 1490 1495 1500
 Ser Leu Cys Val Leu Leu Phe Asp Leu Tyr Asp Gln Leu Thr Leu Ala
 1505 1510 1515 1520
 Asp Arg Lys Gly Glu Asp Phe Ala Leu Gly Ile Glu Arg Leu Ile Pro
 1525 1530 1535
 Leu Phe Gln Thr Cys Ile Ala Gly Ile Leu Asn Ser Asn Ser Thr Pro
 1540 1545 1550
 Ser Leu Arg Ser Asp Leu Tyr Val Val Gly Asn Lys Phe Leu Leu Lys
 1555 1560 1565
 Cys Phe Glu Arg Glu Ser Phe Leu Lys Gln Val Met His Ile Ile Lys
 1570 1575 1580
 Ser Val Asp Lys Lys Phe Phe Gln Val Ile Cys Asn Asp Ala Ile Tyr
 1585 1590 1595 1600
 Ser Glu Gly Pro Ser Arg Ile Thr Ser Thr Leu Phe Leu Glu Ser Leu
 1605 1610 1615
 Val His Leu Gly Thr Leu Val Lys Val Asp Phe Ile Leu Asn Ala Leu
 1620 1625 1630
 Ile Lys Asn Asn Ala Leu Leu Leu Leu Val Arg Ser Val Lys Arg Thr
 1635 1640 1645

Asp Ala Met Ile Lys Leu Cys Gln Glu Lys Asn Ser Gly Val Thr Leu
 1650 1655 1660
 Asp His Phe Ile Phe Asp Leu Met Ala Phe Lys Ala Thr Leu Tyr Phe
 1665 1670 1675 1680
 Phe Val Arg Val Ala Lys Ser Lys Asn Gly Ala Leu Gln Leu Ile Gln
 1685 1690 1695
 Asn Glu Leu Phe Ser Ile Leu His Gln Ser Lys Phe Leu Gln Ile Asp
 1700 1705 1710
 Pro Asp Ile Gly Leu Ser Leu Arg Ile Glu Glu Val Gln Asp His Lys
 1715 1720 1725
 Thr Val Asn Val Asn Val Leu Leu Asp Thr Pro Leu Ser Ile Thr Asp
 1730 1735 1740
 Leu Val Asp Pro Tyr Lys Leu Arg Ser Glu Asn Thr Ile Ser Tyr Phe
 1745 1750 1755 1760
 Glu Phe Leu Val Pro Ile Phe Gln Leu Leu Thr Thr Val Leu Leu Ser
 1765 1770 1775
 Met Gly Pro Asn Tyr Gln Pro Ala Ile Ile Gln Thr Arg Glu Leu Met
 1780 1785 1790
 Lys Ser Val Asn Arg Leu Val Val Gly Val Met Lys Arg Asp Phe Leu
 1795 1800 1805
 Val Glu Thr Lys Gln Ile Gly Gln Gly Leu Tyr Lys Glu Glu Ser His
 1810 1815 1820
 Glu Leu Val Ser Leu Lys Glu Leu Val Lys Leu Phe Ile Leu Ile Asp
 1825 1830 1835 1840
 Ser Leu Ala His Tyr Ser Val
 1845

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<211> 575

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Homologous
 Fragment to Sc YJL039c

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 ttggtacaag gaactcaaaa tatgatatag tgttttcact tcgcaacttg tatggatcca 180
 ccaagtcagt tatcgaaagt ggagtatcta gcaaaacatt tacattgaca gtcttgtgat 240

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cttgaacttc ttcaattcgt aaacttaaac caatatctgg atcaatctgc aaaaacttcg 300
actgatgcaa aattgaaaac aattcatttt ggaatcannn nnanaantna aaaaaaatat 360
atattntntt tttttttttt ttntttnttt tttattttat cttacannac accccaacac 420
aacaccaaac ccnaaaacac ccaacacctc catcttgtcc cgcttttctc tcacattttt 480
tctctactac tatcacacaa tctataaaac atacaccccc tcaaccctc ctccccaaca 540
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<210> 13
<211> 921
<212> DNA
<213> Candida albicans

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<220>
<221> CDS
<222> (1)..(918)

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<220>
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  1              5              10              15

tgg tta cca cca cca cac cca cca aat cct act ggt att gac agt gac 96
Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp
              20              25              30

ccg gct tta gca cca cat ggt gtt gaa caa gcc caa cag tta gct gcc 144
Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala
              35              40              45

tat ctt aca tca tta cct aca cat gaa aag cct gaa ttt att att gct 192
Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala
              50              55              60

tca cct ttt tat cgt tgt ata gaa acg tcg aga ccc att gcc gaa atg 240
Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met
              65              70              75              80

ttg gac ttg aag att gct tta gaa aga gga gtt ggt gaa tgg ttt cgt 288
Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg
              85              90              95

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aaa aat aga gat acc aaa cca gtt ccc ggt gat tac aca caa ttg aga	336
Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg	
100 105 110	
aca ttt ttc gat aaa tta ttg atc gat gaa gat act tgg cca aga gat	384
Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp	
115 120 125	
aac tta aat gtt ata cct aat att gaa gga gaa gat tat gat gaa atc	432
Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile	
130 135 140	
tac gat cgt gcc aaa ttg ttt tgg aaa aag ttt att cct gaa ttt gaa	480
Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu	
145 150 155 160	
aag aaa ttc ccc gaa att aaa aat gtg ttg ata gtt aca cat gca gca	528
Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala	
165 170 175	
acg aaa att gct tta gga tca gct tta tta cag tta aaa tca gtt act	576
Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr	
180 185 190	
gat gtt ata gat gat aat caa act gtg tta cgt gct ggt gca tgt tca	624
Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser	
195 200 205	
tta tcc aaa ttt gtt aga gat ggc gaa gat aaa acc aat cat act att	672
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile	
210 215 220	
caa tgg aaa att gtc atg aat ggt aat tgt gaa ttc ttg aca cag ggt	720
Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly	
225 230 235 240	
gaa gaa atg aac tgg gat ttc cgt cgt ggt gtt gaa gcc ggg tca gct	768
Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala	
245 250 255	
gaa gat ata gcg caa aga aag gca gca gca gaa gca gaa gca aaa gca	816
Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala	
260 265 270	
ttg aag aaa aat gaa caa acc aaa tcc gat ggt ccc atc act gaa tct	864
Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser	
275 280 285	
gcc act ggg gca gaa ata gat ggg aat gaa gat gaa ttt gaa gta cgt	912
Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Val Arg	
290 295 300	

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Lys Thr
305

921

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<211> 306
<212> PRT
<213> Candida albicans

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Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala
35 40 45
Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala
50 55 60
Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met
65 70 75 80
Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg
85 90 95
Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg
100 105 110
Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp
115 120 125
Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile
130 135 140
Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu
145 150 155 160
Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala
165 170 175
Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr
180 185 190
Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser
195 200 205
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile
210 215 220

Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly
 225 230 235 240
 Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala
 245 250 255
 Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala
 260 265 270
 Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser
 275 280 285
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 290 295 300
 Lys Thr
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<210> 15
 <211> 1454
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic splice variant

<220>
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 <222> (1)..(1452)
 <223> gene CaOR110 Splice Variant

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 Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp
 20 25 30
 ccg gct tta gca cca cat ggt gtt gaa caa gcc caa cag tta gct gcc 144
 Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala
 35 40 45
 tat ctt aca tca tta cct aca cat gaa aag cct gaa ttt att att gct 192
 Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala
 50 55 60
 tca cct ttt tat cgt tgt ata gaa acg tcg aga ccc att gcc gaa atg 240
 Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met
 65 70 75 80

ttg gac ttg aag att gct tta gaa aga gga gtt ggt gaa tgg ttt cgt	288
Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg	
85 90 95	
aaa aat aga gat acc aaa cca gtt ccc ggt gat tac aca caa ttg aga	336
Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg	
100 105 110	
aca ttt ttc gat aaa tta ttg atc gat gaa gat act tgg cca aga gat	384
Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp	
115 120 125	
aac tta aat gtt ata cct aat att gaa gga gaa gat tat gat gaa atc	432
Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile	
130 135 140	
tac gat cgt gcc aaa ttg ttt tgg aaa aag ttt att cct gaa ttt gaa	480
Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu	
145 150 155 160	
aag aaa ttc ccc gaa att aaa aat gtg ttg ata gtt aca cat gca gca	528
Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala	
165 170 175	
acg aaa att gct tta gga tca gct tta tta cag tta aaa tca gtt act	576
Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr	
180 185 190	
gat gtt ata gat gat aat caa act gtg tta cgt gct ggt gca tgt tca	624
Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser	
195 200 205	
tta tcc aaa ttt gtt aga gat ggc gaa gat aaa acc aat cat act att	672
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile	
210 215 220	
caa tgg aaa att gtc atg aat ggt aat tgt gaa ttc ttg aca cag ggt	720
Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly	
225 230 235 240	
gaa gaa atg aac tgg gat ttc cgt cgt ggt gtt gaa gcc ggg tca gct	768
Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala	
245 250 255	
gaa gat ata gcg caa aga aag gca gca gca gaa gca gaa gca aaa gca	816
Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala	
260 265 270	
ttg aag aaa aat gaa caa acc aaa tcc gat ggt ccc atc act gaa tct	864
Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser	
275 280 285	

gcc act ggg gca gaa ata gat ggg aat gaa gat gaa ttt gaa aca ttt	912
Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Thr Phe	
290 295 300	
tat gta acc atc gat ata cct tca att tcg aat aaa atc gac aat gaa	960
Tyr Val Thr Ile Asp Ile Pro Ser Ile Ser Asn Lys Ile Asp Asn Glu	
305 310 315 320	
gaa gaa cca cca tca agg aca ggt caa gct cca aaa ttc aaa aac aat	1008
Glu Glu Pro Pro Ser Arg Thr Gly Gln Ala Pro Lys Phe Lys Asn Asn	
325 330 335	
att atc aag cct tca gca caa ctc caa ttt act gat tta aaa gaa gat	1056
Ile Ile Lys Pro Ser Ala Gln Leu Gln Phe Thr Asp Leu Lys Glu Asp	
340 345 350	
cat cca tta gta aaa ata tcg aac aat act ata tct gct caa ggc tcg	1104
His Pro Leu Val Lys Ile Ser Asn Asn Thr Ile Ser Ala Gln Gly Ser	
355 360 365	
tcg tcg tcg tcg tta tca gcg tcg aaa aat gga ttt aat agt cat act	1152
Ser Ser Ser Ser Leu Ser Ala Ser Lys Asn Gly Phe Asn Ser His Thr	
370 375 380	
cac aat tca gga gtc att gat cca tca gca ctt ata gat ggg aaa att	1200
His Asn Ser Gly Val Ile Asp Pro Ser Ala Leu Ile Asp Gly Lys Ile	
385 390 395 400	
tat cag act gat tgg aat caa tta caa ggt act gaa cta ata ttt gat	1248
Tyr Gln Thr Asp Trp Asn Gln Leu Gln Gly Thr Glu Leu Ile Phe Asp	
405 410 415	
gaa aat ggt caa ttt ata ggc aag gtt aag gaa cat ttg act tgc aat	1296
Glu Asn Gly Gln Phe Ile Gly Lys Val Lys Glu His Leu Thr Cys Asn	
420 425 430	
aat aac aca aaa ttc aca tta aaa aag gca gaa gaa gta gaa caa ctt	1344
Asn Asn Thr Lys Phe Thr Leu Lys Lys Ala Glu Glu Val Glu Gln Leu	
435 440 445	
cgt tca gca gat gat tct atc atg gat ata gat caa gac tca caa gga	1392
Arg Ser Ala Asp Asp Ser Ile Met Asp Ile Asp Gln Asp Ser Gln Gly	
450 455 460	
caa caa cca gct aga agt cag ttc tta aaa aga gca att gtg gct gct	1440
Gln Gln Pro Ala Arg Ser Gln Phe Leu Lys Arg Ala Ile Val Ala Ala	
465 470 475 480	
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Arg Ala Lys Gly	

<210> 16
 <211> 484
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic amino acid
 sequence encoded by the splice variant of SEQ ID NO: 15

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Pro	Ala	Leu	Ala	Pro	His	Gly	Val	Glu	Gln	Ala	Gln	Gln	Leu	Ala	Ala	35	40	45	
Tyr	Leu	Thr	Ser	Leu	Pro	Thr	His	Glu	Lys	Pro	Glu	Phe	Ile	Ile	Ala	50	55	60	
Ser	Pro	Phe	Tyr	Arg	Cys	Ile	Glu	Thr	Ser	Arg	Pro	Ile	Ala	Glu	Met	65	70	75	80
Leu	Asp	Leu	Lys	Ile	Ala	Leu	Glu	Arg	Gly	Val	Gly	Glu	Trp	Phe	Arg	85	90	95	
Lys	Asn	Arg	Asp	Thr	Lys	Pro	Val	Pro	Gly	Asp	Tyr	Thr	Gln	Leu	Arg	100	105	110	
Thr	Phe	Phe	Asp	Lys	Leu	Leu	Ile	Asp	Glu	Asp	Thr	Trp	Pro	Arg	Asp	115	120	125	
Asn	Leu	Asn	Val	Ile	Pro	Asn	Ile	Glu	Gly	Glu	Asp	Tyr	Asp	Glu	Ile	130	135	140	
Tyr	Asp	Arg	Ala	Lys	Leu	Phe	Trp	Lys	Lys	Phe	Ile	Pro	Glu	Phe	Glu	145	150	155	160
Lys	Lys	Phe	Pro	Glu	Ile	Lys	Asn	Val	Leu	Ile	Val	Thr	His	Ala	Ala	165	170	175	
Thr	Lys	Ile	Ala	Leu	Gly	Ser	Ala	Leu	Leu	Gln	Leu	Lys	Ser	Val	Thr	180	185	190	
Asp	Val	Ile	Asp	Asp	Asn	Gln	Thr	Val	Leu	Arg	Ala	Gly	Ala	Cys	Ser	195	200	205	
Leu	Ser	Lys	Phe	Val	Arg	Asp	Gly	Glu	Asp	Lys	Thr	Asn	His	Thr	Ile	210	215	220	
Gln	Trp	Lys	Ile	Val	Met	Asn	Gly	Asn	Cys	Glu	Phe	Leu	Thr	Gln	Gly	225	230	235	240

Glu	Glu	Met	Asn	Trp	Asp	Phe	Arg	Arg	Gly	Val	Glu	Ala	Gly	Ser	Ala	
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Glu	Asp	Ile	Ala	Gln	Arg	Lys	Ala	Ala	Ala	Glu	Ala	Glu	Ala	Lys	Ala	
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Leu	Lys	Lys	Asn	Glu	Gln	Thr	Lys	Ser	Asp	Gly	Pro	Ile	Thr	Glu	Ser	
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Ala	Thr	Gly	Ala	Glu	Ile	Asp	Gly	Asn	Glu	Asp	Glu	Phe	Glu	Thr	Phe	
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Tyr	Val	Thr	Ile	Asp	Ile	Pro	Ser	Ile	Ser	Asn	Lys	Ile	Asp	Asn	Glu	
305								310					315			
Glu	Glu	Pro	Pro	Ser	Arg	Thr	Gly	Gln	Ala	Pro	Lys	Phe	Lys	Asn	Asn	
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Ile	Ile	Lys	Pro	Ser	Ala	Gln	Leu	Gln	Phe	Thr	Asp	Leu	Lys	Glu	Asp	
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His	Pro	Leu	Val	Lys	Ile	Ser	Asn	Asn	Thr	Ile	Ser	Ala	Gln	Gly	Ser	
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Ser	Ser	Ser	Ser	Leu	Ser	Ala	Ser	Lys	Asn	Gly	Phe	Asn	Ser	His	Thr	
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His	Asn	Ser	Gly	Val	Ile	Asp	Pro	Ser	Ala	Leu	Ile	Asp	Gly	Lys	Ile	
385								390					395			
Tyr	Gln	Thr	Asp	Trp	Asn	Gln	Leu	Gln	Gly	Thr	Glu	Leu	Ile	Phe	Asp	
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Glu	Asn	Gly	Gln	Phe	Ile	Gly	Lys	Val	Lys	Glu	His	Leu	Thr	Cys	Asn	
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Asn	Asn	Thr	Lys	Phe	Thr	Leu	Lys	Lys	Ala	Glu	Glu	Val	Glu	Gln	Leu	
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Arg	Ser	Ala	Asp	Asp	Ser	Ile	Met	Asp	Ile	Asp	Gln	Asp	Ser	Gln	Gly	
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Gln	Gln	Pro	Ala	Arg	Ser	Gln	Phe	Leu	Lys	Arg	Ala	Ile	Val	Ala	Ala	
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cct gct ggg aaa gca gtg gac aaa aaa ccc aac tcg tcc gag tta agt 96
Pro Ala Gly Lys Ala Val Asp Lys Lys Pro Asn Ser Ser Glu Leu Ser
      20              25              30

tat tta tta tac tat gca tcc act cgt aga gtc aaa tta gaa aag gtg 144
Tyr Leu Leu Tyr Tyr Ala Ser Thr Arg Arg Val Lys Leu Glu Lys Val
      35              40              45

att aat ttt ttg aaa gat aaa act cat cat gat gtt ggt aga aac cgt 192
Ile Asn Phe Leu Lys Asp Lys Thr His His Asp Val Gly Arg Asn Arg
      50              55              60

act ggt aat tta caa gtc aca tta gcc att att cag gaa tta atc aaa 240
Thr Gly Asn Leu Gln Val Thr Leu Ala Ile Ile Gln Glu Leu Ile Lys
      65              70              75              80

aaa tgt agt gaa aac ttg aat gtt ttt gcc ttt caa gtg tgc tat atc 288
Lys Cys Ser Glu Asn Leu Asn Val Phe Ala Phe Gln Val Cys Tyr Ile
      85              90              95

ttg caa ctg att gcc aac act aag gat ctt gcc ttg tgt aaa aat gtt 336
Leu Gln Leu Ile Ala Asn Thr Lys Asp Leu Ala Leu Cys Lys Asn Val
      100              105              110

gtc aaa aca ttt ggt gtt ttg tgt gaa aac ttg gat ggt ggg ttg ttc 384
Val Lys Thr Phe Gly Val Leu Cys Glu Asn Leu Asp Gly Gly Leu Phe
      115              120              125

aca ggt gat aag gag ttt ata aag att ttc act gaa gtt ttc caa aca 432
Thr Gly Asp Lys Glu Phe Ile Lys Ile Phe Thr Glu Val Phe Gln Thr
      130              135              140

tta gtt tcc ttt ggt aag gac aga tcg ggt gtt act cag tat gat tgg 480
Leu Val Ser Phe Gly Lys Asp Arg Ser Gly Val Thr Gln Tyr Asp Trp
      145              150              155              160

cag atg att tct tta atg gct ata aat gat ata tcc agt tgt ttg agt 528
Gln Met Ile Ser Leu Met Ala Ile Asn Asp Ile Ser Ser Cys Leu Ser
      165              170              175

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tat aat gca gct gtt ggt aaa aag ttt att gct ttg tcg att cct gtt	576
Tyr Asn Ala Ala Val Gly Lys Lys Phe Ile Ala Leu Ser Ile Pro Val	
180 185 190	
tta ctt cag ttt att att gca aac aac cca caa agc agc ata ttg caa	624
Leu Leu Gln Phe Ile Ile Ala Asn Asn Pro Gln Ser Ser Ile Leu Gln	
195 200 205	
aga ttg aaa tcg aat ctc cac gtt gaa gat gat ggg aag agg ttg tca	672
Arg Leu Lys Ser Asn Leu His Val Glu Asp Asp Gly Lys Arg Leu Ser	
210 215 220	
cgt gct cat ctg caa aaa tcc cat agc aaa att gcc caa caa att gat	720
Arg Ala His Leu Gln Lys Ser His Ser Lys Ile Ala Gln Gln Ile Asp	
225 230 235 240	
gat gat ttc acc aat gat tct tta acc ttg aca gat atc act gaa aag	768
Asp Asp Phe Thr Asn Asp Ser Leu Thr Leu Thr Asp Ile Thr Glu Lys	
245 250 255	
gca ttt tcg tcg atg aaa tct ttt ttc aat acc aat gct gcc agt caa	816
Ala Phe Ser Ser Met Lys Ser Phe Phe Asn Thr Asn Ala Ala Ser Gln	
260 265 270	
atc tct gaa gtg aca aga gct gtt gtc caa cac aat att ctc aat gga	864
Ile Ser Glu Val Thr Arg Ala Val Val Gln His Asn Ile Leu Asn Gly	
275 280 285	
acc gat ttg gag tgg gga gtc tca ttc ttg gaa tta tgt att act tgg	912
Thr Asp Leu Glu Trp Gly Val Ser Phe Leu Glu Leu Cys Ile Thr Trp	
290 295 300	
att cca gtt caa tta cgt ttt gtc agt ttg tcc acc ttg ttg gcc act	960
Ile Pro Val Gln Leu Arg Phe Val Ser Leu Ser Thr Leu Leu Ala Thr	
305 310 315 320	
tta ggt aga att aat att gaa ggt aac acc aaa tcc aat tac aac atg	1008
Leu Gly Arg Ile Asn Ile Glu Gly Asn Thr Lys Ser Asn Tyr Asn Met	
325 330 335	
caa ttc cag tat gct cgt tac ttg tta gga tta ctt tca tct cgt gtg	1056
Gln Phe Gln Tyr Ala Arg Tyr Leu Leu Gly Leu Leu Ser Ser Arg Val	
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Asn Met Ile Gly Leu Ser Val Ser Asp Ile Ile Gln Gln Leu Leu Ser	
355 360 365	
ttg caa gct gat ttg att ttg aag gca agt gat ttg gac aaa agt gaa	1152
Leu Gln Ala Asp Leu Ile Leu Lys Ala Ser Asp Leu Asp Lys Ser Glu	
370 375 380	

att tca att tta aca gac att tat tct gac tgt att tgt agt ttg act	1200
Ile Ser Ile Leu Thr Asp Ile Tyr Ser Asp Cys Ile Cys Ser Leu Thr	
385 390 395 400	
aca cat ata tat tac ttt gat caa gtc ccg gac tcg att caa gaa atc	1248
Thr His Ile Tyr Tyr Phe Asp Gln Val Pro Asp Ser Ile Gln Glu Ile	
405 410 415	
tta atc aag att gat tac att tta gaa agc agt ttt gtg gaa gat aat	1296
Leu Ile Lys Ile Asp Tyr Ile Leu Glu Ser Ser Phe Val Glu Asp Asn	
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aac att acg tcc act gga gaa caa att caa gat ttg att atc caa ttg	1344
Asn Ile Thr Ser Thr Gly Glu Gln Ile Gln Asp Leu Ile Ile Gln Leu	
435 440 445	
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Leu Asp Asn Ile Ser Lys Ile Phe Leu Ile Leu Lys Asn Lys Ser Ser	
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Ser Ile Asn Arg Asn His Val Asn Leu Glu His Trp Asp Ile Ser Leu	
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Gly Leu Leu Ala Pro Gln Gly Asp His Asp Asp Asn Arg Lys Met Ile	
485 490 495	
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Ile Ser Thr Gln Leu Ile Asn Ile Gln Ala Arg Tyr Leu Lys Val	
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Phe Asp Glu Phe Leu Asn Asn Glu Leu Ala Val Gly Asn Ser Lys Lys	
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Ser Tyr Asp Leu Leu Ser Lys Gln Ser Arg Leu Asp Pro Gly Ser Thr	
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Ala Val Glu Gly Val Asn Lys Ser Asp Asp Leu Asp Asn Gly Lys Asp	
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Phe Lys Lys Pro Asp Ala Asn Gln Tyr Ile Thr Asn Gln Gln Asn Phe	
565 570 575	
ata tcc cat ttc ctt atg tat atc gac aaa ttt ttc gaa aat tac gat	1776
Ile Ser His Phe Leu Met Tyr Ile Asp Lys Phe Phe Glu Asn Tyr Asp	
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Ser	Pro	Asn	Thr	Gln	Ser	Val	Leu	Leu	Leu	Val	Thr	Val	Leu	Lys	Asp	
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Phe	His	His	Trp	Val	Met	Lys	Val	Asn	Arg	Ala	Ser	Asn	Phe	Thr	Gln	
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Arg	Gln	Lys	Phe	Lys	Asp	Thr	Phe	Ala	His	Ile	Ile	Leu	Tyr	Tyr	Met	
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Leu	Lys	Asp	Leu	Asp	Glu	Gln	Tyr	Ser	His	Asp	Leu	Gln	Asn	Tyr	Cys	
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aaa	agc	tct	aaa	tta	ttc	aaa	caa	ata	ttg	gat	gct	gtt	gaa	tat	aga	2064
Lys	Ser	Ser	Lys	Leu	Phe	Lys	Gln	Ile	Leu	Asp	Ala	Val	Glu	Tyr	Arg	
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Lys	Met	Gln	Lys	Phe	Trp	Val	His	Gly	Ile	Asp	Pro	Ser	Pro	Ser	Asp	
	690					695					700					
ttg	gaa	aac	act	aaa	ggc	gac	cgt	acg	ata	ccc	aca	gat	gcc	aat	ggc	2160
Leu	Glu	Asn	Thr	Lys	Gly	Asp	Arg	Thr	Ile	Pro	Thr	Asp	Ala	Asn	Gly	
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aat	tat	att	gct	att	aga	atc	aaa	cct	gaa	aat	att	gag	gaa	ttt	gcc	2208
Asn	Tyr	Ile	Ala	Ile	Arg	Ile	Lys	Pro	Glu	Asn	Ile	Glu	Glu	Phe	Ala	
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tgt	ggc	aac	aac	ttt	ttg	att	gta	tgg	tta	cat	ccc	caa	aaa	caa	tta	2256
Cys	Gly	Asn	Asn	Phe	Leu	Ile	Val	Trp	Leu	His	Pro	Gln	Lys	Gln	Leu	
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ctc	act	gaa	att	gaa	aaa	tca	caa	gtc	agt	act	cat	atg	agc	aca	ttc	2304
Leu	Thr	Glu	Ile	Glu	Lys	Ser	Gln	Val	Ser	Thr	His	Met	Ser	Thr	Phe	
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aat	aat	gat	tct	aga	aac	aca	aat	atg	aca	gtg	ata	atg	gat	caa	gga	2352
Asn	Asn	Asp	Ser	Arg	Asn	Thr	Asn	Met	Thr	Val	Ile	Met	Asp	Gln	Gly	
	770					775					780					
tca	ctg	gca	cta	agt	gga	ggc	gca	gac	cat	gga	ggc	cac	ttt	gtt	ccg	2400
Ser	Leu	Ala	Leu	Ser	Gly	Gly	Ala	Asp	His	Gly	Gly	His	Phe	Val	Pro	
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Ser Asn Ser Glu Lys Gly Leu Tyr Thr Gly Leu Gly Leu Gly Thr Ala	
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Gly Asp Ile Thr Met Ile His Ser Glu Ile Leu Gln Tyr Ser Gln His	
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Phe Gln Glu Arg Gly Leu Pro His Gly Asn Gly Phe Ala Thr Ile Leu	
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cga act gtc gat agt gtt aac agt act aat gat ggg tta att tat act	2640
Arg Thr Val Asp Ser Val Asn Ser Thr Asn Asp Gly Leu Ile Tyr Thr	
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Tyr Asp Ser Lys Tyr Leu Gln Ser Pro Arg Val Ser Asp Leu Lys Asp	
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Ala Met Ser Thr His Arg Gly Ile Arg Leu Ser Lys Pro Asn Phe Gly	
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 Lys Cys Ser Glu Asn Leu Asn Val Phe Ala Phe Gln Val Cys Tyr Ile
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 Ala Phe Ser Ser Met Lys Ser Phe Phe Asn Thr Asn Ala Ala Ser Gln
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 275 280 285
 Thr Asp Leu Glu Trp Gly Val Ser Phe Leu Glu Leu Cys Ile Thr Trp
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 Ile Pro Val Gln Leu Arg Phe Val Ser Leu Ser Thr Leu Leu Ala Thr
 305 310 315 320

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Leu	Ile	Lys	Ile	Asp	Tyr	Ile	Leu	Glu	Ser	Ser	Phe	Val	Glu	Asp	Asn	
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Asn	Ile	Thr	Ser	Thr	Gly	Glu	Gln	Ile	Gln	Asp	Leu	Ile	Ile	Gln	Leu	
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Leu	Asp	Asn	Ile	Ser	Lys	Ile	Phe	Leu	Ile	Leu	Lys	Asn	Lys	Ser	Ser	
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Ser	Ile	Asn	Arg	Asn	His	Val	Asn	Leu	Glu	His	Trp	Asp	Ile	Ser	Leu	
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Ala	Val	Glu	Gly	Val	Asn	Lys	Ser	Asp	Asp	Leu	Asp	Asn	Gly	Lys	Asp	
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Ile	Ser	His	Phe	Leu	Met	Tyr	Ile	Asp	Lys	Phe	Phe	Glu	Asn	Tyr	Asp	
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 645 650 655
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 Lys Ser Ser Lys Leu Phe Lys Gln Ile Leu Asp Ala Val Glu Tyr Arg
 675 680 685
 Lys Met Gln Lys Phe Trp Val His Gly Ile Asp Pro Ser Pro Ser Asp
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 Cys Gly Asn Asn Phe Leu Ile Val Trp Leu His Pro Gln Lys Gln Leu
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 Ser Asn Ser Glu Lys Gly Leu Tyr Thr Gly Leu Gly Leu Gly Thr Ala
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 Phe Gln Glu Arg Gly Leu Pro His Gly Asn Gly Phe Ala Thr Ile Leu
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 Arg Thr Val Asp Ser Val Asn Ser Thr Asn Asp Gly Leu Ile Tyr Thr
 865 870 875 880
 Tyr Asp Ser Lys Tyr Leu Gln Ser Pro Arg Val Ser Asp Leu Lys Asp
 885 890 895

Ala Met Ser Thr His Arg Gly Ile Arg Leu Ser Lys Pro Asn Phe Gly
 900 905 910

Gly Ala Asn Gly Thr Ala Asn Met Thr Asp Ser Ala Ser Thr Ser Asn
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Thr Leu Asp Glu Ile Lys Tyr Ala Met Lys His Val Phe Gln Asp Ala	
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Gln Leu Gly Leu Ala Gly His Arg Lys Leu Val Val Ile Leu Lys Asn	
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Val Phe Lys Lys Ala Ile Glu Leu Asn Gln Ile Asn Phe Phe Ala Met	
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Leu Val Lys Asp Ala Asn Glu Glu Lys Arg Ser Lys Glu Glu Glu Lys	
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Glu Glu Lys Asp Lys Asp Glu Asp Lys Asp Thr Asn Glu Ser Asp Lys	
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Tyr Gly Met Ser Ile Leu Asp Lys Ser Ser Lys Tyr Lys Tyr Ser Arg	
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 Gln Leu Gln Ala Leu Ile Lys Ala Leu Asp Ala Thr Val Glu Leu Phe
 1060 1065 1070

Thr Asn Asn Glu Asp Asn Pro Asn Phe Ile Leu Asp Lys Pro Thr Lys
 1075 1080 1085
 Lys Asn Phe Asp Thr Phe Ile Glu Ser Ile Lys Asn Lys Leu Glu Ile
 1090 1095 1100
 Ala Gln Lys Arg Glu Glu Asn Glu Leu Ile Lys Ser Gly Thr Asn Ser
 1105 1110 1115 1120
 Ile Leu His Glu Leu Asp Asp Leu Asp Ile Gly Thr Gly Glu Ser Ser
 1125 1130 1135
 Gln Ile Ser Ile Lys Ser Glu Thr Lys Arg Arg Asp Leu Asp Arg Ser
 1140 1145 1150
 Leu Gln Val Ser Lys Thr Thr Ser Pro Glu Thr Ser Glu Asn Glu Asp
 1155 1160 1165
 Glu Glu Asp Asp Asn Glu Glu Glu Glu Gln Glu Lys Lys Lys Ser Phe
 1170 1175 1180
 Thr Asp Gly Lys Asn Lys Leu Glu Leu Lys Ala Asp Lys Pro Ile Thr
 1185 1190 1195 1200
 Phe Lys Ala Glu Asp Lys Arg Glu Gly Ser Val Glu Thr Asp His Gly
 1205 1210 1215
 Gln Glu Gln Val Leu Val Glu Ser Lys Lys Val Ile Asp Ser Asn Val
 1220 1225 1230
 Glu Asp Ser Leu Glu Asp Ile Asp Lys Phe Leu Glu Glu Ala Asp Asp
 1235 1240 1245
 Val Asp Tyr Gly Asp Ile Ser Met Asp
 1250 1255

<210> 22
 <211> 603
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Homologous
 Fragment to Sc YDR325

<400> 22
 ctgtttgtta atggtcttgt aaaagatgcc aatgaagaaa aacgttccaa agaagaagaa 60
 aaagaagaga aagacaaaga caaagacaaa gatacgaatg aaagtgataa aatgaagaa 120
 gatcaggaag atcaagaagg agaaggagat caagaaactc caatttcgga attcatatca 180
 tatttgataa aatattttatt gagtgggata gaggctaaag ataaactggt tcgttatcgt 240

gttgtacaaa cattagcata cttggttgaa ttcttgaccg agatacacga gaataataca 300
 ttggaagcgt tatatacttt attaagtaat aggctacaag ataaagagct gtcgatacgt 360
 attcaagctg ttgtggcatt atcacatttt caattatttg aatttagtat tgaaggtgat 420
 actggagaat ttgaggatga attaatatca agtaaccaa ttcagaataa attgataaat 480
 tccattcaaa atgatgatag tccagaagtc agacgtgcag cattaatgaa tttggttaaa 540
 acacaagata caataccgat tttacttgag cgagccagag attccaattc tattaataga 600
 aga 603

<210> 23
 <211> 581
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Homologous
 Fragment to Sc YDR325

<400> 23
 ggggttaaat gatcgtgatg aatctgttaa agcagccgcc tttaaatgc taaccattta 60
 ttggtatcaa tctgtcaatg aagatttatt agaattaatt gatcaattaa atgtcagaag 120
 tgctatagct gaacaggcca tattagcatt ttttaaaaat aaaccagaag ttcttgcaac 180
 tattaataatt gatgaatcat attggaaaaa tctaactaca gaaaaggcat tcttgatgag 240
 gacgttttat caatattgta atgagaatca attacatgct ttaatggatg ccaatttccc 300
 tgaattactt gatttgtcaa taacattaga aaagtatttg tcagtgaggt tgaaaacaat 360
 aaatgaaaat gaaaatttaa ttaagacatg ggaaacttat aatgccaga ttgacgaatt 420
 agatgatcaa atatttagtc ttgaaaacca gatttccaga ataaatactg atgccgataa 480
 tttccgtaaa agtttatcta acattgaaga agatattatt gaaatcaata ttgctaagga 540
 tttgttcaaa aagagaatta aacaattgaa aaactgagca c 581

<210> 24
 <211> 662
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Homologous
Fragment to Sc YDR325

<400> 24

tggtgactca attcatttga tgcacaaaa ttacaatgca ttgtcgctga gtagattatg 60
caaattgttt ttagccgata ttttgtacaa gactgacaaa cggatttatt tggaaatgct 120
attcaagggtg gtgggtgggtg tgatgatcca actaccacca atgacgatga aactgaagaa 180
gaaacagatc gagagcatga aaagcattta tttgaagcga ttgtacttat ttatttcaac 240
cccaacacca aatcaaatca agaattacaa caaattttgt cattttgtat tccagtttat 300
gccttttctc atataaatca tcaaataaat ttagctgcag ttagtggtga tgttatttat 360
cgacttttca ctgaaacaga aacagaatta tcaccaagtg ttataatccc tcaattaata 420
tcattggtgtg atcctcgaaa tttagttaaa ttatcgaatg aggaaataaa tcaagcaaca 480
tcacatttat ggcaatgtgt ttatttatta caagtgggtg aacaagtaga tgctcgtaat 540
gttaaaagat gcatcattaa caatttgaat aaatttcata taacggaaga attagaatca 600
aatcaattac aagctttaat taaagctctt gatgctacag ttgaattatt tactaataat 660
ga 662

<210> 25

<211> 231

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Homologous
Fragment to Sc YOR110

<400> 25

atatgtgttg atagttacac atgcagcaac gaaaattgct ttaggatcag ctttattaca 60
gttaaaatca gttactgatg ttatagatga taatcaaact gtgttacgtg ctgggtgcatg 120
ttcattatcc aaatttggtta gagatggcga agataaaacc aatcatacta ttcaatggaa 180
aattgtcatg aatggtaatt gtgaattctt gacacagggt gaagaaatga a 231

<210> 26

<211> 50

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<220>
 <221> modified_base
 <222> (27)..(32)
 <223> Encompasses variable nucleotides that represent an
 appropriate restriction site

<400> 26
 gagagagaga gagagagaga actagtnnnn nntttttttt tttttttttt 50

<210> 27
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 27
 attcatccca tcagtgcaga aag 23

<210> 28
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 28
 attgaccaat agctctaatt aatg 24

<210> 29
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 29
 agtattcaat tgggtattcc 20

<210> 30
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 30
 ccggcatcat cagtaactcc 20

<210> 31
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 31
 gacgtcgtag acgataactca agaag 25

<210> 32
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 32
 ctgcagtaaa ccctccagat ataacag 27

<210> 33
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 33
 tagctcaacc taccaccaat c 21

<210> 34
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 34
 atcacaagac tgtcaatgta aat 23

<210> 35
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 35
 cggaattcct atcgactacg cgatcatgg 29

<210> 36
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 36
 gcgaattccg atataggcgc cagcaac 27

<210> 37
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 37
 caattgcttt gactcgggtg ttattaagt 29

<210> 38
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 38
tcttggcaca acttgataag aatctgt 27

<210> 39
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 39
taggtgtacg cgaaagccaa gtagaac 27

<210> 40
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 40
ttgttaatcg tacacctaag gtgttgac 28

<210> 41
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 41
ttgcagattg atgctagcaa tgtatttg 28

<210> 42
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 42
 cgggatccgg taaccaattg gatctataac cgtg 34

<210> 43
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 43
 gcggatcctg gtgcccttgg tggatgaatg 29

<210> 44
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 44
 gcggatccct cacaatatga cgattgaaac t 31

<210> 45
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 45
 ggcgtcgact caggcgccag ttttacgtac ttcaaattca tc 42

<210> 46
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 46
 tgtgaattct tgacacaggg tga

23

<210> 47
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 47
 caaaccttca gcacaactcc a

21

<210> 48
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 48
 cacctgtgaa caaccaccca tc

22

<210> 49
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 49
 gaatatcctt tttaactcaa gag

23

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 50
gctttcccag caggataaca ttg 23

<210> 51
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 51
tgagttataa tgcagctggt gg 22

<210> 52
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 52
catctcgtgt gaacatgatt gg 22

<210> 53
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 53
agttttcttca acttccagat ccaag 25

<210> 54
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 54
gtatatttgc aactgtctct ctctc 25

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 55
cgagcatcta cttgttcaac cac 23

<210> 56
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 56
gaatctcttg ctcgctc 17

<210> 57
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 57
gaccgagata caccagaat 19

<210> 58
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 58
 gggttaaata tcgtgatgaa t 21

<210> 59
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 59
 caacctcact gacaaatact t 21

<210> 60
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 60
 acgcttccaa tgtattattc tcg 23

<210> 61
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 61
 ggatgccaat ttccctga 18

<210> 62
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 62
catccagaag atataacggc t

21

<210> 63
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 63
tgcataatct actcagcgc a

21

<210> 64
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 64
gtgggtgaac aagtagatgc tcg

23

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 65
gcgcttgaaa ccactagtga attg

24

<210> 66
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 66
 caattcacta gtggtttcaa gcgc

24

<210> 67
 <211> 133
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 67
 Ile His Pro Ile Ser Ala Glu Ser Leu His Ser His Leu Gln Gln Leu
 1 5 10 15
 Ile Asn Asp Lys Pro Gln Glu Thr Val Gln Glu Ser Ser Asp Leu Leu
 20 25 30
 Gln Phe Ile Pro Val Ser Arg Leu Pro Val Lys Asp Asn Ile Leu Lys
 35 40 45
 Phe Asp Gln Ile Asn His Lys Ser Pro Thr Leu Ile Met Gly Ile Leu
 50 55 60
 Asn Met Thr Pro Asp Ser Phe Ser Asp Gly Gly Lys His Phe Gly Lys
 65 70 75 80
 Glu Leu Asp Asn Ile Val Lys Gln Ala Glu Lys Leu Val Ser Glu Gly
 85 90 95
 Ala Thr Ile Ile Asp Ile Gly Gly Val Ser Thr Arg Pro Gly Ser Val
 100 105 110
 Glu Pro Thr Glu Glu Glu Glu Leu Glu Arg Val Ile Pro Leu Ile Arg
 115 120 125
 Ala Ile Arg Gln Ser
 130

<210> 68
 <211> 200
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Deduced
protein sequence of *Candida albicans* probe of SEQ
ID NO: 1

<400> 68

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Pro Asp Leu Asn Ile Pro His Pro Arg Met Leu Glu Arg Thr Phe Val
 1             5             10             15

Leu Glu Pro Leu Cys Glu Leu Ile Ser Pro Val His Leu His Pro Val
      20             25             30

Thr Ala Glu Pro Ile Val Asp His Leu Lys Gln Leu Tyr Asp Lys Gln
      35             40             45

His Asp Glu Asp Thr Leu Trp Lys Leu Val Pro Leu Pro Tyr Arg Ser
      50             55             60

Gly Val Glu Pro Arg Phe Leu Lys Phe Lys Thr Ala Thr Lys Leu Asp
      65             70             75             80

Glu Phe Thr Gly Glu Thr Asn Arg Ile Thr Val Ser Pro Thr Tyr Ile
      85             90             95

Met Ala Ile Phe Asn Ala Thr Pro Asp Ser Phe Ser Asp Gly Gly Glu
      100            105            110

His Phe Ala Asp Ile Glu Ser Gln Leu Asn Asp Ile Ile Lys Leu Cys
      115            120            125

Lys Asp Ala Leu Tyr Leu His Glu Ser Val Ile Ile Asp Val Gly Gly
      130            135            140

Cys Ser Thr Arg Pro Asn Ser Ile Gln Ala Ser Glu Glu Glu Glu Ile
      145            150            155            160

Arg Arg Ser Ile Pro Leu Ile Lys Ala Ile Arg Glu Ser Thr Glu Leu
      165            170            175

Pro Gln Asp Lys Val Ile Leu Ser Ile Asp Thr Tyr Arg Ser Asn Val
      180            185            190

Ala Lys Glu Ala Ile Lys Val Gly
      195            200

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<210> 69

<211> 293

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 69

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Asn Asp Leu Asn Glu Val Leu Asp Gln Cys Thr Lys Ile Ala Glu Lys
 1             5             10             15

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Arg Leu Gln Leu Gln Asp Gln Ile Asp Gln Glu Arg Gln Gly Asn Phe
 20 25 30
 Asn Asn Val Glu Ser His Ser Asn Ser Pro Ala Leu Leu Pro Pro Leu
 35 40 45
 Lys Ala Gly Gln Asn Gly Asn Leu Met Arg Arg Asp Arg Ser Ser Val
 50 55 60
 Leu Ile Leu Glu Lys Phe Trp Asp Thr Glu Leu Asp Gln Leu Phe Lys
 65 70 75 80
 Asn Val Glu Gly Ala Gln Lys Phe Ile Asn Ser Thr Lys Gly Arg His
 85 90 95
 Ile Leu Met Asn Ser Ala Asn Trp Met Glu Leu Asn Thr Thr Thr Gly
 100 105 110
 Lys Pro Leu Gln Met Val Gln Ile Phe Ile Leu Asn Asp Leu Val Leu
 115 120 125
 Ile Ala Asp Lys Ser Arg Asp Lys Gln Asn Asp Phe Ile Val Ser Gln
 130 135 140
 Cys Tyr Pro Leu Lys Asp Val Thr Val Thr Gln Glu Glu Phe Ser Thr
 145 150 155 160
 Lys Arg Leu Leu Phe Lys Phe Ser Asn Ser Asn Ser Ser Leu Tyr Glu
 165 170 175
 Cys Arg Asp Ala Asp Glu Cys Ser Arg Leu Leu Asp Val Ile Arg Lys
 180 185 190
 Ala Lys Asp Asp Leu Cys Asp Ile Phe His Val Glu Glu Glu Asn Ser
 195 200 205
 Lys Arg Ile Arg Glu Ser Phe Arg Tyr Leu Gln Ser Thr Gln Gln Thr
 210 215 220
 Pro Gly Arg Glu Asn Asn Arg Ser Pro Asn Lys Asn Lys Arg Arg Ser
 225 230 235 240
 Met Gly Gly Ser Ile Thr Pro Gly Arg Asn Val Thr Gly Ala Met Asp
 245 250 255
 Gln Tyr Leu Leu Gln Asn Leu Thr Leu Ser Met His Ser Arg Pro Arg
 260 265 270
 Ser Arg Asp Met Ser Ser Thr Ala Gln Arg Leu Lys Phe Leu Asp Glu
 275 280 285
 Gly Val Glu Glu Ile
 290

<210> 70
 <211> 224
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Deduced
 protein sequence of Candida albicans probe of SEQ
 ID NO: 4

<400> 70
 Lys Ser Ile Gln Leu Gly Ile Pro Ser Asn Lys Lys Lys Asp Arg Ser
 1 5 10 15
 Ser Ile Met Val Leu Lys Lys Met Trp Asp Ser Gln Leu Gln Ser Leu
 20 25 30
 Phe Lys His Val Asp Gly Ala Ser Lys Phe Val Gln Pro Leu Pro Asn
 35 40 45
 Arg His Ile Val Ala Glu Ser Gly Arg Trp Phe Glu Val Asn Val Gly
 50 55 60
 Asn Trp Lys Pro Ser Tyr Pro Thr His Leu Phe Ile Phe Asn Asp Leu
 65 70 75 80
 Ile Leu Ile Ala Val Lys Lys Ser Ser Ser Ser Gln Glu Pro Thr
 85 90 95
 Thr Gly Gly Ser Asn Gly Gly Ser Lys Ser Arg Leu Gln Ala Val Gln
 100 105 110
 Cys Trp Pro Leu Thr Gln Val Ser Leu Gln Gln Ile Lys Ser Pro Lys
 115 120 125
 Lys Asp Asp Asp Lys Met Tyr Phe Ile Asn Leu Lys Ser Lys Ser Leu
 130 135 140
 Ser Tyr Val Tyr Leu Thr Asp Arg Tyr Asp His Phe Val Lys Val Thr
 145 150 155 160
 Glu Ala Phe Asn Lys Gly Arg Asn Glu Met Ile Gln Ser Glu Arg Leu
 165 170 175
 Leu Asp Ser Arg Leu Ser Ser Pro Ser Asn Asn Asn Gly Asp Ser Lys
 180 185 190
 Glu Glu Lys Arg Gln Leu Arg Glu Ser Leu Arg Asn Ser Gly Asn Tyr
 195 200 205
 Lys Glu Gly Val Thr Asp Asp Ala Gly Gly Ala Ala Thr Gly Val Thr
 210 215 220

<210> 71
 <211> 236
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Homologous
 fragment to Sc YOR110

<400> 71
 ttaaatatgt gttgatagtt acacatgcag caacgaaaat tgctttagga tcagctttat 60
 tacagttaaa atcagttact gatgttatag atgataatca aactgtgtta cgtgctgggtg 120
 catgttcatt atccaaattt gttagagatg gcgaagataa aaccaatcat actattcaat 180
 ggaaaattgt catgaatggg aattgtgaat tcttgacaca ggggtgaagaa atgaat 236

<210> 72
 <211> 540
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 72
 acccattgct gaaatgttgg acttgaagat tgctttagaa agaggagttg gtgaatgggtt 60
 tcgtaaaaat agagatacca aaccagttcc cgggtgattac acacaattga gaacattttt 120
 cgataaatta ttgatcgatg aagatacttg gccaaagagat aacttaaatg ttatacctaa 180
 tattgaagga gaagattatg atgaaatcta cgatcgtgcc aaattgtttt ggaaaaagtt 240
 tattcctgaa tttgaaaaga aattccccga aattaaaaat gtgttgatag ttacacatgc 300
 agcaacgaaa attgcttttag gatcagcttt attacagtta aaatcagtta ctgatgttat 360
 agatgataat caaactgtgt tacgtgctgg tgcattgttca ttatccaaat ttgttagaga 420
 tggcgaagat aaaaccaatg atactattca atggaaaatt gtcattgaatg gtaattgtga 480
 attcttgaca cagggtgaag aaatgaactg ggatttccgt cgtggtgttg aagccgggtc 540